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SEARCH REQUEST FORM

Scientific and Technical Information Center

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Art Unit:	Phone Number 30	Serial Number:					
Mail Box and Bldg _i Ro	om Location:	Results Format Preferred (circle):	PAPER	DISK	E-MAII		
If more than one sea	rch is submitted, please	prioritize searches in order of ne	ed.				
Include the elected species utility of the invention. De known. Please attach a cop.	or structures, keywords, synony fine any terms that may have a good the cover sheet, pertinent cl		ombine will citations,	th the cor	cept or		
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Jan Delaval
Reference Librarian
Blotechnology & Chemical Library
CM1 1E07 – 703-308-4498
jan.delaval@uspto.gov

STAFF USE ONLY	Type of Search	Vendors and cost where applicable
Searcher	NA Sequence (=)	SŤN
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Pred. No. is the number of results predicted by chance to have a

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SUMMARIES

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TITLE JOURNAL		Antibodies Patent: US	agair 63126	33.	nman CD4 6 06-NO			

Location/Qualifiers 19.68599 19.68599 19.68599 19.685999 19.6859999 19.68599999999999999999999999999999999999	AAGGACAGGA 	1199 ATTGCGGTCCTCCCAGCTCATTCCCCCCCCCCCCCCCCC	2419 TTACCCTATCATCTTCTCAAGACAGTCCTCCTCAAACCCACAAGCCTTCTGTTCTCTCTC	Db 2659 TGCAACCTGATATTTTTTTTTTTTTTTTTTTTTTTTTTT
Location/Qualifiers 1395 a 2124 c 1980 g 2387 t 1 others 1 Similarity 90.61; Pred, No. 0; Mismatches 137; Indels 49; Gaps 4 2305 ACCATGGATTCACCCCAGGATTCTTATATCCTCTCTCTATCTGGATCTCT 68 2 ACCATGGATTCACCCCAGGATTCTTATATCCTCTCTCTATCTGGATCTCT 68 2 ACCATGGATTCACCCCAGGATTCTTATATCCTCTCTCTATCTGGATCAGATCACCC 106 2 ACCATGGATTCACCCCAGGATTCTTATATCCTCTCTCTCT				
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DEFINITION Homo sapiens genomic DNA, chromosome 2p11.2, clone:cos141. ACCESSION AP001215.3 GI:10121125	Homo sapiens DNA, clone:cos141. Homo sapiens ENkaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia: Crithoria: Drimator: Craniata; Vertebrata; Euteleostomi;	rammaira; bucheria; Filmaces; Cacarrinis; Hominidae; Homo. 1 Shimizu,N. and Kawasaki,K. Homo sapiens genomic DNA, chromosome 2p11.2, clone:cos141	AL Published Only in Database (2000) CE 2 (bases 1 to 37201) RS Shimizu,N. and Kawasaki,K.	yoshi Shimizu, Keio University, School	Tel-8502, udpan (E-mail:nShimizh@dmb.med.Kelo.ac.jp, Tel:81-3-3351-2370, Fax:81-3-3351-2370) COMMENT On Sep 13, 2000 this sequence version replaced gi:8096503. FEATURES Location/Onalifiers	ce 1. 37201 /organis="Homo sapiens"	158.4F001215." 9606."	/map="zpii.z" /clone="cosi41" repeat region 184: 492	/evidence=not_experimental /rpt_family="Alux" /rpt_family="Alux"	/er/is 123/ /er/dence=not_experimental /rpt_family="AT_rich"	ental	tal .	8258 8394 /evidence=not_experimental /rpt_family="WLT1C"	83999007 /evidence=not_experimental /rpt_family="LIMD2"	9017. 19170 evidence=not_experimental rpt_family="L1MD3"	91899529 /evidence=not_experimental /rpr_family="MLTIC"	ental	ental	region 10763. 10936 /evidence=not_experimental /rpt_family="GA-rich"	region 11443 .11600 /evidence=not experimental /rpt_family="MIR"	region 11733. 12023 /evidence=not_experimental /rpt_family="MRR33"	ental	/evidence=not_experimental /rpt_family="AT_rich"

6101 GGAGAAGTGCCCCACCTGCTCCTCAGCCTGACCCCCTCCCATCCTTTGGCCTC 6160 1153 TGACCTTTTTCCACAGGGACCTACCCTATTGCGGTCCTCCAGCTCATTTTTTTT	1453 CCCTCAAACCCAAACCTTCTTCTCTCAAACCCTGGGCCATGGTAGGAACACTCT 6460 6461 CCCTCCAAACCCACAAGCCTTCTGTCCTCAACCCCTGGGCCATGGTAGGAAGACTTG 1512 6461 CCCTCCAAACCCACAAGCCTTCTGTCCTCTTTTAAAGGCTAGGAAGACTTG 6520 1513 CTTCCTTGTTTTCCCCTCCTCAGCAAGCCTCTTTTTAAAGGTAACAACATTG 6520 1573 ACAGCATTTTTCCCTCCTCAAGCAAGCCTCATAGTCCTTTTTAAAGGTAACAAGTTT 1572 6521 CTTCCTTGTTTTCCCTCCTCAAGCAAGCCTCATAGTCCTTTTTAAAGGTACAAAGGTCTT 1572 6521 CTTCCTTGTTTTCCCTCAAGCAAGCCCTCATAGTCCTTTTTAAAAGGTAACAAGTTTTTCAAAAG 1632 1633 AAAAACCTGCTATAAAAAAAAAAAAATCCCTCAAAAAAAA	821 AGGGCGTATTGAGTACTTTCCACAACCTTAN 873 AACATTCATTAAAATGTTGCAAAGGTTCTAT 881 AACATTCATTAAAATGTTGCAAAGGTTCTAT 882 AACATTCATTAAAATGTTGCAAAGGTTCTAT 883 TCAGCAATCCCACTTCTAG 1951 941 TCAGCAATCCCACTTCTAG 6959 AC104601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            * NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is
                                              Waterston, R.H.
Direct Submission
Submitted (13-DEC-2001) Genome Sequencing Center, Washing University School of Medicine, 4444 Forest Park Parkway, MO 63108, USA
                                                                                                                                                           Center: Washington University Genome Sequencing Center
Center code: WUGSC
                                                                                                                                                                                                                                                                            Sequencing vector: M13; 0%
Sequencing vector: M13; 0%
Sequencing vector: plasmid; 100%
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 165062 bases at least 040
Consensus quality: 165366 bases at least 030
Consensus quality: 165346 bases at least 030
Insert size: 166000; agarose-fp
Insert size: 166000; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality coverage: 6.84 in Q20 bases; agarose-fp Quality coverage: 6.81 in Q20 bases; sum-of-contigs
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77.4%; Score 1517.4;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1518; Conservative 0; Mismatches
The sequence of Homo sapiens clone Unpublished

2 (bases 1 to 166276)
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                                                                 145044 TACTTAAACACCATCCTGTTTGCTTCTTCCTCAGGAACTGTGGCTGCACCATCTGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             145224 GGGTAACTCCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGAACAGCACCTAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        145584 GIGAATCTTTGCACCTGTGGTTTCTCTCTTTCTCTCTTTAATAATTATTATTGTTGTTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      145644 TACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTAGTCATCCTAAGGGCGATAA
144744 AATTCTAAACTCTGAGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTT
                                                                                                                                                     144924 TITAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTTCTG
                                                                                                                                                                                                                                                                                                                                       144984 TCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACAACACCCCAAGGGCAGAACTTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     145284 CAGCACCCTGACGCTGAGGAAAGCAGACTACGAGAAACACAAAAGTCTACGCCTGCGAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CACCCATCAGGGCCTGAGCTCGCCCGTCACAAGAGCTTCAACAGGGGGAGAGTGTTAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           145344 CACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGAGTTTAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  145464 IGACCCTTTTTCCACAGGGACCTACCCTATTGCGGTCCTCCAGCTCATCTTTCACCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAATTTAGAACTTTAATAAGGAATAGGGGGAAGCTAGGAAGAACTCAAAACATCAAGAT
                                                                                                                                                                                                                  TITIAAATACGCTICTIGGICTCCTIGCTATAATIAICIGGGATAAGCAIGCTGTTTTCIG
                                                                                                                                                                                                                                                                                                     TCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACCCCAAGGGCAGAACTTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAAGGTGGATAACGCCCTCCAATC
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                                          ACTGCAAGGTCAGAAAAGCATGCAAAAGCCCTCAGAATGGCTGCAAAAAGAGCTCCAACAAAA
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Grewal, N. and Abbort, A.

The sequence of Homo sapiens BAC clone RP11-601N4

Unpublished (2001)

Waterston, R. H.

Direct Submission

University, School of Medicine, 4444 Forest Park Parkway, St. Louis, Modille, Universiton, R. 101555)

Waterston, R. H.

Submitted (01-MAR-2002) Department of Genetics, Washington University, A444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Sep 18, 2001 this sequence version replaced gi:7705152.
                                                                                                         146063
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                                                                                                                           AATGGAATGTCATGCCTTATTTACATTTTTAAACAGGTACTGAGGGACTCCTGTCTGCCA 1812
                                                                                                                                                                       AGGGCCGTATTCAGTACTTTCCACAACCTAATTTAATCCACACTATACTGTGAGATTAAA 1872
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AC096579 AC022416
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Catarrhini, Hominidae, Homo.
AAGAAACCTGCTATAAAGAGAATCATTCATTGCAACATGATATAAAATAACAACACAATA
                                                                          AAAGCAATTAAATAAACAAACAATAGGAAAATGTTTAAGTTCATCATGGTACTTAGACTT
                                                                                                                                                                                                                     AACATTCATTAAAATGTTGCAAAGGTTCTATAAAGCTGAGAGACAAATATATTCTATAAC
                             AAGAAACCTGCTATAAAGAGAATCATTCATTGCAACATGATATAAAATAACAACACAATA
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Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Ve
Mammalia; Eutheria; Primates; Catarrhini;
I (bases I to 176555)
Sulston, J. E. and Materston, R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
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D. Louis
                                                                                                                                           This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Oscegawa, K., Woon, P.Y., Zhao, B., Frengen, E. Tateno, M., Catanese, J.J., and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries Genomics 51:1-8 The Clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org
NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-450E9; the clone sequenced to the right is RP11-685N3. Actual start of this clone is at base position 1 of RP11-601N4; actual end is at base position 176555 of RP11-601N4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Data from AC062029 and AC060807 was used to finish this clone, AC023416. Polymorphisms have been identified between AC023416 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (NID:g1437298) zh81a02.rl"
                                                                                                                                                                                                                                                                                                                                                                   MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Mo. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence of AC023416 has been incorporated into AC096579.
Location/Qualifiers
1. 17/6527
/ craanisme="Homo sapiens"
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/ chromosome="2"
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/rpt family="MER1_type"

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/rpt family="1153"
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/ppt family="L1"
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/note="match to EST AN
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/note="match to EST BK
3289. 3365
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942. .2293
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TITLE An analysis of EcoRI/XhoI 3 kb fragment sequence of Nasopharyngeal Carcinoma transforming gene JOURNAL Unpublished REPERSENCE 3 (bases 1 to 7810) AUTHORS Wei, R., Ming, L., Linging, X., Xinxian, W., Wei, L. and Ya, C. TITLE From a nasopharyngeal carcinoma cell line CNE2 JOURNAL Unpublished REFERENCE 4 (bases 1 to 7810)		JOURNAL Submitted (19-AUG-1999) Molecular Biology Laboratory, Cancer Research Institute of Hunan Medical University, 88 Xiangya Road, Changsha, Hunan 410078, People's Republic of China REFERENCE 6 (bases 1 to 7810) AUTHORS Wei,L., Ming,L., Wei,R., Xinxian,W., Lingqin,X. and Ya,C. TITLE Direct Submission JOURNAL Submitted (13-OCT-2000) Molecular Biology Laboratory, Cancer Research Institute of Hunan Medical University, 88 Xiangya Road,	Changsha, Hunan 410078, People's Republic of China REMARK Sequence update by submitter REFERCE 7 (bases 1 to 7810) AUTHORS Wei,L., Ming,L., Wei,L. and Ya,C. TITLE Direct Submission JOURNAL Submitted (10-APR-2002) Molecular Biology, Cancer Research Institute, Xiangya Medical School of Central South University, 88 Xiangva Road. Changsha, Hunan 410078, People's Republic of China	REMARK Sequence update by submitter COMMENT On Jun 26, 2002 this sequence version replaced gi:10800410. FEATURES Location/Qualifiers source 1. 780 Homo sapiens" /db_xref="taxon:9606" /chromosome="2"	/map=".zpl2" /cell_libl2" /tissue_type="nasopharyngeal carcinoma" repeat_region 1499 /rpt_family="Alu-Y" /rpt_type=dispersed		/note="15" /note="15" isc_feature 3583. 463 /note="Reg hancer 4663. 451 region 5411591 JUNT 2423 a 1520 c	Ouery Match Best Local Similarity 99.8%; Pred. No. 0; Matches 1516; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	ATTCTAAACTCTGAGGGGTCGGATGACGTGGCCATTCTTGCCTAAAGCATTGATTTTTTTT
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Burkly,L.C., Chisholm, P.L., Thomas, D.W., Rosa, M.D. and Rosa, J.J.
Antl-CD4 antibody homologs useful in prophylaxis and treatment of
AIDS, ARC and HIV infection
Patent: US 5871732-A 54 16-FEB-1999;
Location/Qualifiers
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1151 TCTGACCCTTTTTCCACAGGGACCTACCCCTATGCGGTCCTCCAGCTCATCTTTCCAC 1224	REBULT 9 AR035238 LOCUCS LOCUCS LOCUCS DEFINITION SEQUENCE 55 from patent US 5871732. ACCESSION AR035238 AR035238 AR035238 AR035238 AR035238 AR035238 AR035238.1 GI:5951906 ARCHWORDS Unknown. REFRENCE Unknown. AUTHOR ALL:CD4 anti-CD4 antibody homologs useful in prophylaxis and treatment of AlD5, ARC antibody homologs useful in prophylaxis and treatment of AlD5, ARC antibody homologs useful in prophylaxis and treatment of AlD5, ARC antibody homologs useful in prophylaxis and treatment of AlD5, ARC antibody homologs useful in prophylaxis and treatment of AlD5, ARC antibody homologs useful in prophylaxis and treatment of AlD5, ARC antibody homologs useful in prophylaxis and treatment of AlD5, ARC antibody homologs useful in prophylaxis and treatment of AlD5, ARC antibody homologs useful in prophylaxis and treatment of AlD5, ARC antibody homologs useful in prophylaxis and treatment of I.1.7701 AUTHOR ALD5, ARC antibody homologs useful in prophylaxis and treatment of I.1.7701 AUTHOR ALD5, ARC antibody homologs useful in prophylaxis and treatment of I.1.7701 AUGHON ALCORATION (Qualifiers out) ALD5, ARC ALCORATION (QUALIFIER) AUGANISM AUTHOR ALD5, ARC antibody homologs useful in prophylaxis and treatment of I.1.7701 AUTHOR ALTON (QUALIFIER) AUGANISM AUTHOR ALD5, ARC ALGA GGCCCAGACTCCAGACTCCAGACTCCCAGACCACAGACTCCCAGACCACAGACTCCAGACTCCCAGACTCCCAGACTCCCAGACTCCCAGACTCCCAGACACTCCCAGACTCCCAGACACTCCCAGACTCCCAGACACTCCCAGACACTCCCAGACACTCCAGACTCCCAGACACTCCAGACTCCAGACTCCCAGACACTCCAGACTCCCAGACTCCCAGACACTCCAGACTCCCAGACACTCCAGACTCCCAGACTCCCAGACTCCCAGACTCCCAGACTCCCAGACTCCCAGACTCCCAGACTCCCAGACTCCCAGACTCCCAGACTCCCAGACACTCAGACTCCCAGACTCCCAGACACTCGCCACACTCGCCCAGACTCCCAGACCCCAGACTCCCAGACCCCAGACTCCCAGACTCCCAGACACTCCAGACTCCCAGACACTCCCAGACTCCCAGACTCCCAGACCCCAGACTCCCAGACTCCCAGACTCCCAGACCCCAGACTCCCAGACACTCCAGACTCCCAGACTCC
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131 CANTAGAGGETCOCCAGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
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λO	1271 AAGTGAATCTTTGCACCTGTGGTTTCTCTCTTTCTCTC-ATTTAATAATAATTATTATG 1329
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λo	1330 TTTTACCAACTACTCAATTTCTCTTATAAGGGCTAAATATGTGTGTCGTCTAAGGGGCA 1389
qq	1345 -TTTACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCA 1403
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λo	1570 CTTACAGTCATATATCCTTTGATTCCATTCCCTGGGAATCAACCAAAGCAAATTTTTCAA 1629
qa	1584 CTTACGGTCATATATCCTTTGATTCCCTGGGAATCAACCAAGGAATTTTTCAA 1643
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VERSION KEYWORDS SOURCE	X6785 Ig ka Homo
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REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1. (bases 1 to 5364)
AUTHORS	Garrard, W.T. Direct Submission
AL	Submitted (23-JUL-1992) W.T. Garrard, UT Southwestern Medical Contre, Department of Biochemistry, 5323 Harry Hines Blvd., Dallas
REFERENCE AUTHORS	1A 5235, USA 2 (bases 1 to 5364) Whitehurer, C., Henney, H.R., Max, B.E., Schroeder, H.W. Jr.,
	Stuber, F., Siminovitch, K.A. and Garrard, W.T.
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Burkly, L.C., Chisholm, P.L., Thomas, D.W., Rosa, M.D. and Rosa, J.J.
Anti-CD4 antibody homologs useful in prophylaxis and treatment of
AIDS, ARC and HIV infection
Patent: US 5871732-A 53 16-FEB-1999;
Location/Qualifiers
     5293 TACGGTCATATATCCTTTGATTCAATTCCTGGGAATCAACCAAGGCAAATTTTTCAAAA
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Qy B55 ATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGATGAACGCCTCCAATCGG 914 Db 444 ATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGATGCATACGCCTCCAATCGG 503 Qy 915 GTAACTCCCAGGAGAGTGTCACAGACAGCACAGCACCACCCTCAGCA 974 Db 504 GTAACTCCCAGGAGAGTGTCACAGACAGACAGACACACCCTCAGCA 563 Qy 975 GCACCCTGAGGAAGAGAACAGAACACAAAGCACAAAAGCACAAAAAGCACAAAAGCACAAAAAA	OY 1035 CCCATCAGGCCTGAGCTCGCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAGGG 1094	OY 1155 ACCCTTTTCCACAGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTCACCTCAC 1214 Db 744 ACCTTTTTCCACAGGGACCTACCCTATTGCGGTCCTCCAGCTCATCTTCACCTCAC OY 1215 CCCCTCCTCCTCTGCTTTATTATTATGTGGAGGAGAAATGAATAAAAAAAT 1274 Db 604 CCCCTCCTCCTCTTGGTTTTAATTATGTTGGAGGAGAAATGAAAAAAAA		Db 983 CATTATAAAAATCATCCTTCTATTTACCCTATCATCCTGGAAGACAGTCCTC 1042 1454 CCTCAAACCCAAGCCTTCTGTCTCCTGGAGCCATGGTAGGAAGACTTGC 1513 1161 11		HERUKT 12 HSIGKI LOCUS LOCUS LOCUS DEFINITION C-terminal part of human kappa-immunoglobulin gene coding for amino acids 109 to 214. ACCESSION VOOS57 JUG241 VOOS57 JUG131140 SET IN 10 SAPPA LINE, 19 KAPPA LIGHT CHAIN; immunoglobulin. KEYWORDS SOURCE HOWO Sapiens EUKATYOCA, METAZOA; CHORdata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhin; Hominidae, Homo. (Dases 1 to 1209) REFERENCE (Dases 1 to 1209) TITLE Cloned human and mouse kappa immunoglobulin constant and J region

key from to description POLYA 833 833 poly adenylation site CDS 36 653 reading frame. CDS Location/Qualifiers 1.1209 /organism="Homo sapiens" //db_xref="taxon:9606" //map="2pl2" //tissue_type="placenta" //germline	John No. 1325 . 1:1 199,1	/ ACOCOL STATE 32 A 232 C 234 S 325 COUNT 320 A 330 C 234 S 325 C 234 S 235 C 235	Match Local Similarity 99.6%; Pred. No. 7.1e-270; Local Similarity	0y 495 TGCAAGGTCAGAAAGCATGCAAAGGCTCCAAAGGCTCCAACAAACA
Db 661 AGAAGTGCCCCACCTGCTCCAGTTCCAGCCTGACCCCTCCCATCCTTTGGCCTCTG 720 1155 ACCTTTTCCACAGGGGCCTACCCTTTGCGGTCCTCCAGCTCTTTCACCTCAC 1214	841 GAATCTTTGCACCTGTGGTTTCTCTTTCCTCATTTAATAATATTATCTGTTG-TTT 1334 ACCAACTACTCATTTCTCTTATAAGGGACTAAATATTATGTGTTG-TTT 1304 ACCAACTACTCATTTCTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCATAAC 900 ACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCATAAC	QY 1394 CATTATADAAAATCATCATTCATTTTACCCTATCATCCTGCAAGACAGTCCTC 1453 Db 960 CATTATAAAAATCATCCTTCATTCTATTTACCCTATCATC	Dp 1080 TTCCTTGTTTTCCCTCAGGAGCCCTCATAGTCCTTTTTAAGGGTGACAGGTTT 1139	SULT 13 MICKC3 MICKC3 HUMICKC3 FINITION Human 1g germlin 700241.1 G1:185 FINITION J00241.1 G1:185 FINITION Germlin FINITION Germlin FINITION GERMLIN FOR GERMLIN FOR AMAX GIONER HICET. P.A., MAX GIONENAL GERMLIN GERMLIN GERMLIN GERMLIN GERMLIN GERMLIN GOTHER GIOLOGO GUIN GHAMENT G12.2 (1 Pt. 1) FERRENCE 1 (Dases 1 to 1) FERRENCE 2 (Dases 1 to 1) FERRENCE 2 (Dases 1 to 1) FERRENCE 2 (Dases 1 to 1) FERRENCE 3 (Dases 1 to 1) FERRENCE 4 (Dases 1 to 1) FERRENCE 6 (Dases 1 to 1) FERRENCE 6 (Dases 1 to 1) FERRENCE 7 (Dases 1 to 1) FERRENCE 7 (Dases 1 to 1) FERRENCE 6 (Dases 1 to 1) FERRENCE 6 (Dases 1 to 1) FERRENCE 7 (Dases 1 to 1) FERRENCE 6 (Dases 1 to 1) FERRENCE 6 (Dases 1 to 1) FERRENCE 7 (Dases 1 to 1) FERRENCE 7 (Dases 1 to 1) FERRENCE 6 (Dases 1 to 1) FERRENCE 7 (D

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1574 CAGTCATATATCCTTTGATTCCAATTCCCTGGGAATCAAAGCAAAGTTTTTCAAAAGA
                    1163 CGGTCATATATCCTTTGATTCCATGGGAATCAACCAAGGCAAATTTTTCAAAAGA
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Direct Submission
Submitted (21-MAR-1996) C. Hilger, Centre Hospitalier, 4 Rue
Barble, L-1210 Luxembourg, LUXEMBOURG
Related sequences V00557 and J00241.
Location/Qualifiers
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/product="kappa light chain constant region"
/note="C-terminal"
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/dev_stage="adult"
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/clone="pBkappa5"
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Location of Sapiens and Canadata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E. 1 (Abases 1 to 672)

E. Kim, N. S., Hahn, Y., Oh, J. H., Lee, J. Y., Ahn, H. Y., Chu, M. Y., Kim, M. R., Oh, K. J., Cheong, J. E., Sohn, H. Y., Kim, J. M., Park, H. S., Kim, S. and.

Kim, Y. S.

21C Frontier Korean EST Project 2001

Unpublished (2002)

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Fax: +82-42-860-4470

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Copyright (c) 1993 - 2003 Compugen Ltd.
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VENTY TON, J. H., Lee, J. Y., Ahn, H. Y., Chu, M. Y., Kim, M.

NENAL

Oh, K. J.; Cheong, J. E., Sohn, H. Y., Kim, J. M., Park, H. S., Kim, S. and

Wim, Y. S.

TITLE

JIC Frontier Korean EST Project 2001

Vignous Research Center

Gonome Research Center

Korean Research Center

Fax: 1860-4409

Fax: 482-42.860-4409

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Frail Hondon Sapiens

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K-EST0087997 S16N667673 Homo sapiens CDNA clone S16N667673-2-G02
5', mRNA sequence.
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota, Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                  / Jab host="ToploF'"
/ Jab host="ToploF'"
/ Inote="Organ: Stemach; Vector: pCNS; Site 1: EcoRI;
Site 2: NoII; The poly (A) + RNA was dephosphorylated with
batte_2: NoII; The poly (A) + RNA was dephosphorylated with
tabacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dT-selected mRNA by
priming with dT-tailed vector. The dT-tailed vector was
adjusted to have about 60nt. The CDNA vector was
circularized with E. coll DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Toplof' by electroporation method.
The CDNA libraries constructed by this method are
full-length enriched CDNA library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 CTGTCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACCACAAGGCAGAACTT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 GCTGAATAACTTCTATCCCAGAGGCCAAAGTACAGTGGAAGGTGGATAAAGCCCTCCA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   910 ATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCT 969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 ATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGGACAGGACAGCACCTACAGCCT 360
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organism="Homo sapiens"
db_xref="taxon:9606"
clone="S19N665307-2-D11"
clone_lib="S19N665307"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases I to 552)
Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Endocrine Pancreas Consortium
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Endocrine Pancreas Consortium
Barvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: dmelrom@biohp.harvard.edu
Library was constructed by Dr. J. Ferrer In vivo mass-excised to
DBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington
University Genome Sequencing Center For information on obtaining
clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
Seq primer: -40Up from Gibco
High quality sequence stop: 448.
5
220 CAATTTAGAACTTTATTAAGGAATAGGGGAAGCTAGGAAGAAACTCAAAACATCAAGAT
                                                                  TITAAATAGGTITCITGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCTG
                                                                                                                                                                                                                                                                                                                                 GAATAACTICTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATC
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                                                                                                                    TCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACCCCCAAGGGCAGAACTTTGT
                                                                                                                                        TCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACCCAAGGGCAGAACTTTGT
                                                                                                                                                                                        TACTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTT
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                                                                                                                                                                                                                                                                                               CATCTTCCCGCCATCTGAGGGGGGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCT
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5633978"
/clone=lib="Human insulinoma"
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BMS10472.1 GI:18681615
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Fax: 617-495-8557
Email: dmelton@bio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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(http://genome.wustl.edu/est/lambda_protocol.shtml).

Please contact Hiroshi Inoue, MD/PhD for further information on this library (Metabolism Division, Permutt Laboratory, Washington University School of Medicine, Box 8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this is Washington University Pancreas EST project library."

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/tissue_type="insulinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: pancreas; Vector: pBluescript SK-; Site_1:
/note="Organ: pancreas; Vector: pBluescript SK-; Site_1:
Xhol; Site_2: EcoRI; Constructed with lambda ZAPII system
(Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
pBluescript SK- by Dr. H. Inoue following the Washington
University protocol
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Homo sapiens

Homo sapiens

Homo sapiens

Homo sapiens

Homo sapiens

Homo sapiens

Mammaliab Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 557)

Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.

Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and

Kim, Y.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTGGAGGAGAATGAATAAAGTGAATCTTTGCACCTGTGGTT 1294
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K-EST0051794 S14K402 Homo sapiens cDNA c
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BM768769
BM768769.1 GI:19098384
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Home sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammaila; Euthheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 610)

S NIH-MGC http://mgc.nci.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be http://image.llnl.gov

Plate: LLAMISO7 row: p column: 13

High quality sequence stop: 595.

Location/Qualifiers

1. 610

/ organism="Homo sapiens"
/ clone="Homo sapiens"
/ clone="Homo sapiens"
/ lab.hoge:="Maxon:9606"
/ clone="Homo sapiens"
/ lab.hoge:="Maxon:"Homo sapie
                                                                                                                                                                                                                                                          BQ049622 610 bp mRNA linear EST 29-MAR-2002 620 degenCOURT 7077241 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:5787516 5', mRNA sequence.
BQ049622 1 GI:19808962 EST.
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26.6%; Score 521.8; DB 14; Length 610;
Best Local Similarity 99.6%; Pred. No. 7e-97;
Matches 523; Conservative 0; Mismatches 2; Indels 0; Gaps
                                                                                                                              human.
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Best Local S
Matches 523
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Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).
                                                                                                                                             189 ACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGGA 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Euteleostomi;
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Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                 249 GGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGAACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                       309 CGAGAAAACACAAAAGTCTACGCATGCGAAGTCACCCATCAGGGCCTGAGGTCGCCCGTCAC
                                                                                                                                                                                                                          GGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGCATA
                                                                                                                                                                                                                                                                                                                                                                                            CGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            489 ATTGCGGTCCTCCAGCTCATCTTTCACCTCACCCCCTCCTCCTCCTTGGCTTTAATTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  549 GCTAATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGNCCCT 594
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.

CE 1 (bases 1 to 643)

National Libra; Metale, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Mark Watson

CONA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The 1.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the 1.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM2471 row: d column: 01

High quality sequence stop: 594.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1246 AATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCTGT 1290
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Location/Qualifiers

1. 549

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2. crganism="Homo sapiens"

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         Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 540.

NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

Nutional Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: capabs-r@mail.nih.gov.

The sequence contained an olispo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A trail. Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M.B. Soares Lab

CDNA Library Preparation: M.B. Soares Lab

CDNA Library Preparation: M.B. Soares Lab

Clome distribution: MGC clome distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:

Www.bio.llnl.gov/bbrp/image/image.html

Seg primer: Ml3 Forward
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modified polylinker; Site 1: ECOR I; Site 2: Not I;
UI-CF-EC1 is a normalized CDNA library containing the
following tissue(s): Normal lung from adult and from fetal
day 64, day 87, week 19 and week 42. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome. Research, 6:791-806, 1996. First strand CDNA
Synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded CDNA was ligated to an ECOR I
adaptor, digested with Not I, and cloned directionally
into pT773-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand CDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
AAGTCCTTAC.
TAG ILB-UI-CF-ECI
TAG ILB-UI-CF-ECI
TAG ILSSUE=Normal Lung Epithelial Cells Tissue nos 369-371
and 380-383.
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CDNA clone
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Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
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Gaps 0; 481

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/organism="Homo sapiens"
/db xref="taxon:9606"
/db xref="IMAGE:6279733"
/clone="IMAGE:6279733"
/clone lib="NMHH MGC 113"
/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
RCORI; DNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGENCOURT 8353549 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6279733 57, mRNA Fequence.
BQ706352.
BQ706352.1 GI:21845251
EST.
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                1006 GAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAA 1065
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
I (bases 1 to 927)
INH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
   Tissue Procurement: Dr. Mark Watson
   CDNA Library Preparation: Rubin Laboratory
   CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
   DNA Sequencing by: Agencourt Bioscience Corporation
   Clone distribution: MGC clone distribution information can be
   found through the I.M.A.G.E. Consortium/LLNL at:
   http://image.llnl.gov
   Plate: LLCM2469 row: m column: 14
   High quality sequence stop: 658.
                                                                                                                                                                                                                  396 GAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAAGTGCCCCCCACCTGCTCCAGGTTCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                516 GCGGTCCTCCAGCTCATTCACCTCCACCCCCCTCCTTGGCTTTAATTATGCT
                                                             336 GAAACACAAAGTCTACGCCTGCGAAGTCACCCCATCAAGGCCTGAGCTCGCCCGTCACAAA
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Pred. No. 1.5e-96;
0; Mismatches 8; Indels
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                                                                                                                                                                                                                                                                                BQ062789 641 bp mRNA linear EST 02-APR-2002
AGENCOURT 6826785 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5924314
5,, mRNA Sequence.
BQ062789
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
cDNA Library Preparation: Rubin Laboratory
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I:M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I:M.A.G.E. Consortium/LLNL at:
http://image.llh.gov
Plate: LLCM2094 row: d column: 11
High quality sequence start: 77
High quality sequence stop: 596.
Location/Qualifiers
Free I: 641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96 AcGAACTGTGCCACCATCTGTCTTCCCCCCCCCCATCTGATGAGCAGTTGAAATC 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 641)

NIH-MGC http://mgc.nci.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC)
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1246 AATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCT 1288
                                                                                      18
                                                     60 AATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCT
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Best Local Similarity 99.4%;
Matches 522; Conservative (
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TITLE
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RESULT 11 BM509302/c LOCUS DEFINITION SOURCE

ACCESSION VERSION KEYWORDS REFERENCE AUTHORS

TITLE JOURNAL COMMENT

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/organism="Homo sapiens"
//dref = axon:660"
/clone lib="Human insulinoma"
/clone lib="Human insulinoma"
/clone lib="Human insulinoma"
/lab_bost="BilosUlinoma"
/lab_bost="B
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 643)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26.5%; Score 519.8; DB 13; Length 563; 99.4%; Pred. No. 1.8e-96; tive 0; Mismatches 3; Indels 0;
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BQ573939/c
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Bukaryota; Merazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (Dases 1 to 563)

1 (Dases 1 to 563)

2 Melton, D. Brown, J. Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A., Schiller, J., Marcan, R., Cole, R., Tsagareishvili, R., Williams, T., Jackson, Y. and Bowers, Y.

1 Jackson, Y. and Bowers, Y.

1 Endocrine Pancreas Consortium

1 Unpublished (2000)

1 Unpublished (2000)

1 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue Endocrine Pancreas Consortium

1 Contact: Douglas Melton, Klaus H. Kaestner, of Hiroshi Inoue Endocrine Pancreas Consortium

1 Contact: Douglas Melton, Klaus H. Saedical Institute

1 Endocrine Pancreas Consortium

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                                                                                           490 AGCAGTIGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAG
                                                                                                                                                                                                                                   AAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCT
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                                             AGCAGITGAAATCIGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAG
                                                                                                                                                                                          AGGCCAAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTG
                                                                                                                                                                                                                                                                                                                                   TCACAGAGCAGGACAGCACAGGACCTACAGCCTCAGCAGCACCCTGACGCTGAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BM509302.1 GI:18680445
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1065

1005

302

422 945 362

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1125

182

242

1185

1245

62

source

FEATURES

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/note="Vector: pT713-Pac; Site_1: Not1; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA (1.5-2.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento. Soares, Ph.D."
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AWS75927 618 bp mRNA linear EST 15-MAR-2000
UI-HF-BL0-acl-e-02-0-UI.s1 NIH_MGC_37 Homo sapiens cDNA clone
IMAGE:3059426 3', mRNA sequence.
                                                                                                                 1186 GCGGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTTGGCTTTAATTATGCT 1245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs r@mail.nih.gov

The sequence contained an oligo-dT track that was present in the oligonuclectide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. Tissue Procurement: Louis M. Staudt, M.D., Ph.D. cDNA Library Preparation: M.B. Soares Lab cDNA Library Arrayed by: M.B. Soares Lab DNA Sequencing by: M.B. Soares Lab Clone distribution: MGC clone distribution information can be
                124 GCGGTCCTCCAGCTCATTTTTCACCTCACCCCCTCCTCCTTCGTTTAATTATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              754 GCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 618)
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                                                                                                                                                                                                                                      1246 AATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCTGTG 1291
                                                                                                                                                                                                                                                                                       AATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCTGTG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Consortium/LLNL at
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/cell_line="MGC85"
/lab_host="DH10B (LTI)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  found through the I.M.A.G.E. Consortiu
www.bio.llnl.gov/bbrp/image/image.html
Seq primer: Ml3 Forward
PoLYA=Yes.
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/organism="Homo sapiens"
/dx xref="taxon:9606"
/clone="IMAGE:3059426"
/clone=lib="NIH MGC 37"
/tissue_type="lymph"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
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//dev stage="Definition of the property of 
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CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu

POLYA-Yes.
                                                                       Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Steven Gitelis/ Rush Presbiterian, Dept. of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      825
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                   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/dlone="url-H-BZO-bax-d:24-0-UI"
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/tissue_type="Chondrosarcoma Grade II"
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Pred. No. 2e-96;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ocation/Qualifiers
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26.5%;
Best Local Similarity 99.2%;
Matches 522; Conservative
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AUTHORS
TITLE
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766 AGGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGGCCATCTGATGAGGAGTTGAAATC 825
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UJ-HF-BLO-acv-b-06-0-UI.sl NIH_MGC_37 Homo saplens CDNA clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human.
Homo sapiens
Eukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryotta; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NIH-MGC http://mgc.nci.nih.gov/.

Nitional Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-refamail.nih.gov
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
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128 CCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCTTGGC 69
                                    368 CACAGAGGACAGGACGAGGACCTACAGCTCAGCACCTGAGCTCAGGCAGCACGCTGAGGCA 309
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NOI CGAP Cart is a CDNA library containing the following tissue(s): Osteoarthritic Cartilage The library was constructed according to Bonaldo, Lennon and Soares synthesis was primed with an oligo-dr primer containing a genome Research, 6:791-806, 1996. First strand CDNA Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally
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Constructed from size fractionated cytoplasmic, mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
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tail. Tissue Procurement: Louis M. Staudt, M.D., Ph.D. CDNA Library Preparation: M.B. Soares Lab CDNA Library Arrayed by: M.B. Soares Lab DNA Sequencing by: M.B. Soares Lab Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward
POLYA=Yes:
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Minimum DB Maximum DB

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Monoclonal antibody, Hu266, nootropic; neuroprotective, Abeta peptide, Alzheimer's disease, Down's syndrome, cerebral amyloid angiopathy, light chain; ds, gene therapy.
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Expression vector
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pMDR1006 insert.
Vector pMDR1007.
Plasmid pAH4611.
pMDR986 insert. S
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Plasmid pD16hJ1.L1
                                                                                                                                                       July 18, 2003, 04:14:58; Search time 508.109 Seconds (without alignments) 8686.944 Million cell updates/sec
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                   GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
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Listing first 45 summaries
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Result Š.

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                GATGTGGGGAGTTTATTACTGTTCTCAAAGTACACATGTTCCGTGGACGTTCGGTCAAGGC
                                                                GCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAACAATTTAGAACTTTATT
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                                                                                                                                                                                                                                                                                                                                                                                       The invention relates a humanised antibody that specifically binds an epitope contained within positions 13-28 of amyloid beta peptide, Abeta. The antibody is useful to inhibit and reduce the formation of amyloid plaques or the effects of toxic soluble Abeta species in humans their fragments are used for the manufacture of a medicant. This includes the prolonged expression of recombinant sequences of them in human tissues for the treatment of clinical/pre-clinical Alzheimer's disease, Down's syndrome or pre clinical/pre-clinical Alzheimer's disease, Specifically, the antibody is used to sequester Abeta into plasma, brain or cerebrospinal fluid to prevent freverse accumulation of the Abeta sequence encodes the light chain of a humanised monoclonal antibody, Hu266, based on the mouse antibody 266.
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/number= 1
/note= "The figure indicates that the intron
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reading frame of the second exon and is possibly a
mistake by the authors"
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Vasquez M;
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2000US-0254465.
2000US-0254498.
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P-PSDB; AAU07744.
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                                                                                 The sequence is that of a plasmid expressing a structurally altered BR96 antibody, having the variable region of BR96 and a modified variable region. It can be used in the production of the structurally altered antibodies which are useful for the treatment of cancer and carcinomas in vivo, especially when conjugated to cytotoxic agents. Structurally altered BR96 Ab is used, especially conjugated to doxorubicin, to treat proliferative type diseases where a cell has a BR96 antigen on the cell surface. The chimeric and humanised BR96 Ab are also used in the methods to inhibit and prevent BR96-induced toxicity resulting from immunotherapy
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 immuno:therapy - by administration of immunoglobulin fusion modified prior to administration by inactivation of part of
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                                                         Disclosure; Pages 58-60; 140pp; English.
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82.9%; Score 1625.8; DB 19;
Best Local Similarity 91.6%; Pred. No. 0;
Matches 1774; Conservative 0; Mismatches 137; In
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2179 ATTGCGGTCCTCCAGCTCATCTTTCACCTCACCCCCCCTCCTCCTTGGCTTTAATTAT
                                                    CTCAGGAACTGTGGCTGCATCTGTCTTCATCTTCCGGCCATCTGATGAGCAGTTGAA
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                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents an expression vector for expressing the light chain of a chimeric anti-CD40 antibody designated chi220. The antibodies are effective in modulating humoral immune response against T cell dependent antigens, collagen induced arthitis and transplant induced rejection. They are also useful for their anti-inflammatory properties. The antibodies have wide therapeutic applications, including autoimmune and inflammatory diseases and transplantation. The antibody can be used in a pharmaceutical composition for treating a patient suffering from a T cell mediated disorder. They can also be used to treat autoimmune diseases, inflammatory diseases, and transplantation.
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82.2%; Score 1611.8; DB 20; Length 8858;
Best Local Similarity 90.6%; Pred. No. 0;
Matches 1783; Conservative 0; Mismatches 137; Indels 49; C
                                                                                                                                                                                                                                                                                                          Antibody that binds human CD40, for treating T cell mediated disorders
                                                                                                                                                                                                                                         KK, Harris LJ, Hollenbaugh Watkins JD, Wu H;
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Location/Qualifiers
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Huse WD, Siadak AW, Thorne BA,
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                                                                                   2779 AAACAGGTACTGAGGGACTCCTGTCTGCCAAGGGCCGTATTGAGTACTTTCCACAACCTA
                                                                                                                                                                                 2539 TCATAGTCCTTTTTAAGGGTGACAGGTCTTACAGTCATATATCCTTTGATTCAATTCCCT
                                      ATGTTTAAGTTCATGGTACTTAGACTTAATGGAATGTCATGCCTTATTTACATTTTT
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                                                                                                                                                                    "Start codon of inserted signal sequence"
                                                                                                                                                                                                    TAAAGCTGAGAGACAAATATATTCTATAACTCAGCAATCCCACTTCTAG 1951
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HOLLENBAUGH
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BERRY K K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence shows the expression vector encoding the light chain of the chimerised anti-human monoclonal antibody (mAb), Chi220. Chi220 binds to human CD40 (or its active portion). It comprises murine variable and human kappa and gamma I constant regions. It binds to CD40 and effectively blocks humoral immune responses to T cell-dependent antigens in a dose dependant fashion. The antibodies of the invention are useful for modulating humoral immune responses against T cell-dependent antigens, collagen induced arthritis, and skin and kidney transplant rejection and are also useful for their anti-inflammatory properties. They are useful for treating autoimmune disease such as type I diabetes, psoriasis multiple sclerosis, rheumatoid arthritis,
                                                                                                                                                                                                                                                                                                                                                                    New humanized anti-human CD40 antibodies which block interaction between gp39 and CD40 for modulating humoral immune responses against T cell-dependent antigens, collagen induced arthritis, and transplant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            129 ACTATTAGCTGCAAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAGAACTACTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 ACCATGGATTCACAGGCCCAGGTTCTTATATTGCTGCTGCTATGGGTATCTGGCACCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGGGACATTGTGCTGACACAGTCTCCAGATTCCCTGGCTGTAAGCTTAGGAGAGAGGGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1224 TCCATCTCTGGGATCCCCTCCAGGTTCAGTGGCAGTGGATCAGGGTCAGATTTCACTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------AGTCTTCTCAACTCTAGAATTCTAAACTCTGAGGGGGTCGGATGACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 systemic lupus erythematosus and myasthenia gravis, inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 8858;
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                                                                                                                                                                                                     Berry KK, Harris
Watkins JD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8858 BP; 2396 A; 2124 C; 1950 G; 2387 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1611.8; DB 24; Lengt
Pred. No. 0;
); Mismatches 137; Indels
                                                                                                                                                                                                  AW, Be:
Wu H,
                                                                                                                                                                                                  D, Siadak Huse WD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 2; Fig 14; 54pp; English.
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90.6%;
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Bajorath J,
THORNE B A.
BAJORATH J.
HUSE W D.
WU H.
                                                                                                                                      WATKINS J D.
                                                                                                                                                                                                                                                                                                     WPI; 2002-024899/03.
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Sat

1030 1150 1210 1224 1270 1284 1329 1344 1389 1403 1449 1463 1509 1569 1629 1523 1643 1045 Greacecarcadedereadecreececereadadesecreeadedegadegrerrad 1104 910 970 850 864 924 984 804 1450 CCTCCCTCAAACCCACAAGCCTTCTCTCTCACAGTCCCCTGGGCCATGGTAGGAGAGAC
1464 CCTCCCTCAAACCCACAAAGCCTTCTGTCCTCACAGAGTCCCTGGGCCGTGGTAGGAGAGAC TCTGACCCTTTTTCCACAGGGACCTACCCTATTGCGGTCCTCCACTTTTCACC 1165 TCTGACCCTTTTTCCACAGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTCACC 1271 AAGTGAATCTTTGCACCTGTGGTTTCTCTCTTTCCTC-ATTTAATAATTATTATCGTTG 1285 AAGTGAATCTTTGCACCTGTGGTTTCTTTCTTTCCTCAATTTAATAATTATTATTGTTGTTG 1584 CTTACGGTCATATATCCTTTGATTCCCTGGGAATCAACCAAGGCAAATTTTTCAA GITACTIAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTC TTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTG CTGAATAACTTCTATCCCAGAGGCCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAA CTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAAGGGGGATAACGCCCTCCAA TCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGGACAGCACCTACAGCCTC GTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAGAGCTTCAACAGGGGAGAGTGTTAG 1330 TITIACCAACTACTCAATITCTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCA 1524 rigerrecrierrirececrecreadeaacecrearagrecrirrraagggreaggr TCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTC 1510 TIGCTICCTIGITITCCCCTCCTCAGCAAGCCCTCATAGICCTTITIAAGGGTGACAGGT CTTACAGTCATATATCCTTTGATTCCAATTCCCTGGGAATCAACCAAAGCAAATTTTTCAA TTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGT 1630 AAGAAGAACCTGCTATAAAGAGAATC 1656 AAGAAGAACCIGCGGCCGATCGATIC 1670 BP. entry) 02-APR-1993 (first 1225 1570 1644 AAQ30920 745 791 805 851 865 911 925 1031 1151 1211 AAQ30920; AAQ30920 ID AAQ3 XX AC AAQ3 XX DT 02-A XX DE Vect RESULT 셤 g 요 g g g g a q ò ò 임 ò g ò g ò ò ò ઠે 8 ò g ò ò Op ò Dp ò ò

Vector pMDR1007

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The sequence given is the insert of the vector pWDR1007. pWDR1006

(see AAQ30919) and pSAB132 (see AAQ30906) were used in the construction of this vector. Three fragments were ligated together to generate this vector. Three fragment of pWDR986 (see AAQ30913), a 3442bp AatII/

ECORV fragment of pWDR986 (see AAQ30918) and a 326 bp ECORV/BgIII of ECORV fragment of pWDR1006 was used to transform E. Coli JA221(Jq) to ampticillin resistance. pWDR1006 was transform E. Coli JA221(Jq) to ampticillin resistance. pWDR1006 was cleaved with Norl and the 1693 bp fragment isolated was ligated into Norl linearised pSAB132 which had been dephosphorylated by calf alkaline phosphatese. This generates the plasmid pMDR100? The melting agarcse and used to transform E. Coli JA221(Iq) to ampticillin resistance. The pWDR1007 insert comprises DNA encoding, in a 5' to 3' order, the immunoglobulin kappa chain signal peptide, amino acid (AA) cresistance. The pWDR1007 insert comprises DNA encoding, in a 5' to 3' order, the immunoglobulin kappa chain signal peptide, amino acid (AA) cresistance. The pWDR1007 insert comprises DNA encoding plate chain constant region (LC). The polypeptide encoded by genomic DNA encoding AA108-AA214 of the human kappa light chain, ie the light chain constant region (LC). The polypeptide encoded by pMDR1007 is an antibody homolog which was shown to bind to cota but did not block the binding of gg120 to CD4. CD4 is a cells! The homolog clocked HIV-induced syncytia formation. This homolog can be used in the detection, prophylaxis and treatment of diseases caused by
Plasmid; pMDR1006; pSAB132; vector; pMDR1007; pMDR985; AatII; ECORV; pMDR986; BglI; pMDR1003; JAS2I(IQ); E. Coll; ampiciallin resistance; NotI; dephosphorylate; Calf; alkaline phosphatase; low temperature; melting agarose; immunoglobulin; kappa chain; signal peptide; LC; humanised; SAB; light chain; variable region; LV; genomic; constant antibody; homolog; CD4; gpl20; cell surface; glycoprotein; CD4+; lymphocyte; helper; inducer; HIV; syncytia; formation; ss.
                                                                                                                                                                     Location/Qualifiers
35..100
/*tag= a
/note= "Immunoglobulin kappa chain signal sequence"
101...101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New anti-CD4 antibody homolognes - which bind CD4, do not block binding of HIV gpl20 to CD4 but block HIV-induced syncytia formation between CD4+ cells
                                                                                                                                                                                                                                                                                                                                                                  435.

/*tag= d
/number= 1
782.1101
/*tag= e
/number= 2
'~re= "AA108-AA214 of human kappa LC'
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                                                                                                                                                                                                                                                                                   Rosa JJ,
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438..781
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P-PSDB; AAR28809.
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                                                                                                                                                               GGACATTGTGCTGACACAGTCTCCAGATTCCCTGGCTGTAAGCTTAGGAGAGAGGGCCAC
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                                                                                                                                                                                                                     TATTAGCTGCAAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAGAGAACTACTTGGC
                                                                                                                                                                                                                                             160 TATAAACTGCAAGTCCAGTGGGAGCCTTTTATATAGTACCAATCAAAAGAACTACTTGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 925 TCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTC
                                                                                                           CATGGATTCACAGGCCCAGGTTCTTATATTGCTGCTGTTGGGTATCTGGCACCTGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                         371 TTACACGTTCGGACAGGGGACCAAGGTGGAAATAAAACGTAAGTAGTCTTCTCAACTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAAATTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGT
                                                     13; Length 1701;
                         Seguence 1701 BP; 435 A; 469 C; 361 G; 436 T; 0 other;
 CD4+ cells.
                                                                                97;
                                                     DB
                                                   Score 1427.8;
Pred. No. 0;
0; Mismatches
infective agents whose primary targets are
                                                   Query Match
Best Local Similarity 93.1%;
Matches 1533; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents the expression vector pAH4611.

This vector was produced from the plasmid pA64270. pA64270

This vector was produced from the plasmid pA64270.

It is the expression vector for the light chain variable region (VL) of the antibody 128.1 which was obtained by PCR with leader/J region priming (see also AA043842). The vector also contains an ampicillin resistance gene, a gpt (mycophenolic acid resistance) selected marker, an immunoglobulin H enhancer and an intron for V-constant region splicing.

C Transcription of the CH gene is from the VH promoder of the murine 27.44 gene. The cloning of the 128.1 VL region was accomplished in two stages with the production of plasmid pS44271 as an intermediate vector which lacks the promoter region. This plasmid was used in conjunction with pAH4602 in the production of the chimeric antibody which binds to the transferrin receptor on brain capillary endothelial cells. This antibody may be used in a conjudate in which it is invested to a neuropharmaceutical or disagnestic agent. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 14; Length 13999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antibody conjugates specific for transferrin receptor - used for diagnosis and treatment of cancer, AIDS and neurological
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60.4%; Score 1184.2; DB 99.5%; Pred. No. 4e-268; ive 0; Mismatches 4
                                                       /*tag= d
/note= "Undefined ORF"
9300..12092
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920..7218
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8424..8741
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Best Local Similarity 99.5
Matches 1208; Conservative
                                                                                                                                                                                                                                                                                                                          (ALKE-) ALKERMES INC
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P-PSDB; AAR41686-87.
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                 985 AGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAAGTCTACGCCTGCGAA
                                                     GTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAGAGCTTCAACAGGGGAGAGTGTTAG
                                                                                1045 GTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAG
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                                                 3507 GAATAACTTCTATCCCAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATC
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TACTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTT
                                                                              CATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCT
                                                                                                                     GAATAACTICTAICCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAAIC
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The sequence given is the insert of the intermediate plasmid pMDR986.

DMDR996 was constructed to carry genomic DNA encoding amino acid (AA) and the sequence but as constructed to a human kappa light chain ie. the light chain onstant region (LC). Human placental genomic DNA was prepared and cleaved with EcoRI to give a 2.5 Kb fragment. This fragment comprising the with EcoRI to give a 2.5 Kb fragment. This fragment comprising the kappa chain constant region was cloned into the EcoRI site of pUGB to give pABB. The DNA encoding LC was amplified from pABB using the primer sequences given in AAQ30914-15. The 1240 bp reaction product was ligated into EcoRV linearised pNN03 (see AAQ30565) that had been dephosphorylated. This generated plasmid pSAB153 (see AAQ30916). LC was amplified from pSAB153 using the primers given in AAQ30915 and AAQ30917 to generate an approx. 1276 bp fragment. This fragment was igated to EcoRV linearised pNN03 that had been dephosphorylated by the presence of a 1122 bp Ecololo9 I restriction fragment. E. Coli GA22(IG) to ampliciallin resistance. Plasmid pMNR986 was used to transform E. Coli GA229, which does not methylate its own DNA. Sequence analysis of pMDR986 showed that a cloning artifact caused a NorI site 3' of the constant region to be been replaced with a Pvul site.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New anti-CD4 antibody homolognes - which bind CD4, do not k
binding of HIV gp120 to CD4 but block HIV-induced syncytia
formation between CD4+ cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rosa MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 161-2; 205pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rosa JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91WO-US08843.
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                                                                                                  02-APR-1993 (first entry)
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                                                                                                                                                                pMDR986 insert.
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                               AAQ30918;
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83

614

AAQ30918 standard; DNA; 1276

RESULT 9 AAQ30918 ID AAQ3

BP.

entry)

(first

02-APR-1993

AAQ30916;

pSAB153 insert.

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AAQ30916 standard; DNA; 1241

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                                                                                                    TGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACCCCAAGGGCAGAACTTTGTTA
                                                      204 TAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCTGTC
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                                 TAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCTGTC
                                                                                                                                                                           CTTAAAACACCATCCTGTTTGCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTTCA
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                                                                                                                                                                                                                                                                                   384 TCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGA
                                                                                                                                                                                                                                                                                                                     ATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGG
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The sequence given is the insert from the intermediate plasmid pSAB153.

This plasmid was used in the construction of the intermediate plasmid pNASP86 (see AAQ30918). pWDRP866 was constructed to carry genomic DNA encoding amino acid (AA) 108-AA214 of a human kappa light chain ie.

The light chain constant region (LC). Human placental genomic DNA was prepared and cleaved with ECORI to give a 2.5 kb fragment. This fragment comparising the kappa chain constant region was cloned into the ECORI site of pUCB to give pAB8. The DNA encoding LC was amplified from pAB8 using the primer sequences given in AAQ30914-15. The 1240 bpth cartion product was ligated into ECORY linearised plasmid pSAB153 and that had been dephosphorylated into ECORY linearised plasmid pSAB153. LC was amplified from pSAB153 using the primers given in AAQ30915 and AAQ30917 to generate an approx. 1276 bp fragment. This fragment was ligated to ECORY linearised pNN03 (see AAQ30566) that had been dephosphorylated by calf alkaline phosphatase. The ligation mixture was used to transform E. coli JA221(Iq) to ampicillin resistance.

Chamand pMDR986 was identified by the presence of a 1122 bp Ecol109 I restriction fragment. pWDR986 was used to transform E. coli GM2929, which does not methylate its own DNA. Sequence analysis of pMDR986 showed that a cloning artifact caused a Not1 site 3' of the constant
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                                                                                                                                                                    plasmid; pMDR986; genomic; DNA; human; kappa; light; chain; constant; region; LC; placenta; EcoRI; pUC8; pAB8; EcoRV; pNN03; pSAB153; dephosphorylated; calf; alkaline phosphataes; E. coli; JA221(Iq); EcoU109 I; E. coli; GM2295; methylate; cloning artifact; NotI; PvuI; CD4; CD4; HIV; gpl20; syncytia; formation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 TICTAAACTCTGAGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New anti-CD4 antibody homolognes - which bind CD4, do not block binding of HIV gp120 to CD4 but block HIV-induced syncytia formation between CD4+ cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2,
                                                                                                                                                    polymerase chain reaction; PCR; amplify; intermediate;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thomas
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99.6%; Pred. No. 8.4e-268;
ive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rosa MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    region to be been replaced with a PvuI site.
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                                                                                                                                                                                                                                                                                                                                                                                                                 91WO-US08843.
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Matches 1205;
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                                                                                                                                                                                                                                                                                           Synthetic.
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Sequence 3880 BP; 981 A; 1013 C; 921 G; 965 T; 0 other;
                                                                                                                              Plasmid pCK7-96 nucleotide sequence.
                                                                              AAV39242 standard; DNA; 3880 BP
                                                                                                                                                                                                                                                              97WO-US21803.
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                                                                                                              (first entry)
                      1634 AGAAACCTGC 1643
                                  1223 AGAAACCTGC 1232
                                                                                                                                                                                                                                                                                              (GENP-) GENPHARM INT.
                                                                                                                                                                                                                                                                                                                             WPI; 1998-333306/29.
                                                                                                                                                                               ARDS; vasculitis; se
cystic fibrosis; ss.
                                                                                                                                                                                                                                                                                                              Kay RM, Lonberg N;
                                                                                                                                                                                                     Synthetic.
Homo sapiens.
                                                                                                                                                                                                                              WO9824884-A1.
                                                                                                                                                                                                                                                              01-DEC-1997;
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                                                                                                               18-DEC-1998
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       1163
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864 GAATCTTTGCACCTGTGGTTTCTCTCTTTTTTTAATTATTATTATGTGT-TTT 922
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                                                                                                                                                              TCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTTGTTGTGTGCCTGCTGA 854
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The present sequence represents the kappa light chain plasmid, pCK7-96, which includes the kappa constant region and polyademylation site. The plasmid is used in the construction of miniganes for expression of igdkappa anti-CD4 antibodise, in the transgenic mouse of the invention. Igdkappa anti-CD4 antibodise, in the transgenic mouse of the invention. The specification describes transgenic non-human animals, especially a mouse, which are capable of producing a buman heterologous antibodies of multiple isotypes by undergoing isotype switching. The transgenic animals of functionally rearranging at heterologous diversity (D) gene in a heavy chain transgene comprising at least one V, D and J gene segment, and one constant region gene segment. The immunoglobulin (ig) light chain transgene comprises at least one V, D and J gene segment, and one constant region gene segment. The immunoglobulin (ig) light chain region gene segment are new escenter and one constant region gene segment are new constant and one constant region gene segment are new or constant and one constant region gene segment are new or constant and also be used to prevent efflux of neutrophils from an also be used to treat repetition injury. The antibodies are used to reduce undesirable autoimmune reactions, inflammatory responses and reduce itssue damage and prolong survival in animal models of acute adult respiratory discress syndrome (ARDS) and and induced lung injury. The anti-IL-8 antibodies can also be used for the treatment of vascultitis, septic shock, allergic reactions
Transgenic animal; human heterologous antibody; transgene; isotype switching; neutrophil efflux; reperfusion injury; CD4 binding; autoimmune reaction; inflammatory response; transplant rejection; acid induced lung injury; acute adult respiratory distress syndrome; ARDS; vasculitis; septic shock; allergic reaction; asthma;
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smatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          composition has been developed which comprises an immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                            Ig; affinity constant; human; antigen; hybridoma; B cell; transgenic; mouse; CD4; antibody; autoimmune; inflammatory; transplant rejection; immunoglobulin; ss.
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Pred. No. 2.3e-235;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                              Kappa light chain plasmid pCK7-96
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nent of auto-immune disease
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Homo sapiens.
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                                                                                                                                                         Novel transgenic non-human animals used to antibodies
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                                                                                 99WO-US05535.
                                                                                                                             conberg N, Fishwild DM,
                                                                                                              (GENP-) GENPHARM INT INC.
                                                                                                                                            WPI; 1999-551219/46.
                                                   WO9945962-A1
                                                                                12-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The specification describes transgenic animals that are capable of producing a heterologous antibody. The antibodies are isolated form a hybridoma, comprising B cells, that is obtained from a transgene made having a genome comprising a human heavy chain transgene and a human light chain transgene. The B cells are fused to immortalized cells suitable for generating a hybridoma, which produces a detectable amount of an immunoplobulin that specifically binds digoxin or Shinga-like toxin. B cells from transgenic animals can be used to generate hybridomas expressing monoclonal high affinity human sequence antibodies. Antibodies produced from the transgenic animals of the invention can be used to treat human diseases, cancer, infectious diseases, transplant rejection, blood diseases, cancer, infections disorders and other diseases. The present sequence is used in the course of the invention.
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human light chain transgene; immortalized cell; immunoglobulin;
Shinga-like toxin; autoimmune disease; cancer; infectious disease;
transplant rejection; blood disorder; coagulation disorder; ss.
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Bost Local Similarity 99.8%; Pred. No. 2.3e-235;
Matches 1066; Conservative 0; Mismatches 0; Indels 2;
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CAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGT 1032
                                                                                                                                                                                                                       The present invention relates to novel transgenic nonhuman mammals, particularly rodents, comprising two human immunoglobulin (1g) loci, where one of two the human immunoglobulin loci is a human heavy chain locus and the other locus is a human light chain locus, and where one of the loci is of a transchromosome. The transgenic animals are useful for generating a number of B-cell expressing human antibody sequences. They are also useful for producing rearranged immunoglobulin sequences, producing human antibody display libraries, and generating a human sequence antibody that binds to a predetermined antigen. The produced antibodies are useful for treating immune related disorders. The present sequence represents a plasmid used in the
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                                                                                                              New transgenic nonhuman mammal, useful for generating B-cells expressing human antibody sequences and generating antigen-specific hybridomas secreting human sequence antibody, comprises two human
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Pred. No. 2.3e-235;
0; Mismatches 0;
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                  (KIRI ) KIRIN BEER KK
     MEDAREX INC.
                                                                                 WPI; 2002-500300/53
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                                                                                                                                                                                                                                                                                                                      NB: Humanised anti-CD18 Ab 60.3 variable light chain (pGk.11) sequences are given in Fig 10 and Sequence ID 10 of the specification; corresp. to AAQ62611 and AAQ55004 respectively.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Monoclonal antibody; MAb; heavy chain; light chain; constant region; variable region; amplification; primer; polymerase chain reaction; PCR; chimera; Ig; integrin; ss. immunoglobulin; humanised antibody; leucocyte; integrin; ss.
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by computer database searching
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AAQ55004 standard; DNA; 7059 BP.
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Chimeric: Mus sp.
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These two sequences are not identical; AAQ55004 comprising 7059 bases and AAQ65211 comparising 8400 bases. Fig 10 should consist of and pages (1/4, 2/4, 3/4 and 4/4), however, page 2/4 is duplicated and pages 4/4 is missing. The sequence found in AAQ62611 represents pages 1/4 - 3/4.

The sequence found in AAQ62611 represents for and pages 1/4 - 3/4.

A humanised monoclonal antibody corresponding to the murine anti-CD18 artibody 60.3 was prepared. The variable (V) regions security of an applicated onto human constant (C) regions, resulting in a chimeric 60.3 Ab (1991, kappa). The chimeric Ab was resulting in a chimeric 60.3 Ab (1991, kappa). The chimeric Ab was competition and inhibition assays showed that the chimeric Ab was competition and inhibition assays showed that the chimeric Ab was sefective as the murine 60.3 MAb. The deduced murine W and VL protein sequences were selected to be used as and two human 1g protein sequences were selected to be used as and two human 1g protein sequences were selected to be used as chuman template sequences selected from the protein data base, and humanised frow was modeled. Construction of the humanised 60.3 was construction of the humanised 60.3 were again constructed that the humanised Ab (1991, kappa). The humanised proteins were again constructed that the humanised 60.3 Ab master wells were transferred and assaved for The humanised 60.3 Ab master wells were transferred for the advanced for The humanised 60.3 Ab master wells were transferred for the advanced for The humanised 60.3 Ab master mells were transferred for the advanced for The humanised 60.3 Ab master mells were transferred for the advanced for The humanised 60.3 Ab master mells were again to the founce for the humanised 60.3 Ab master mells were transferred for the founce for th
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Best Local Similarity 98.1%; Pred. No. 2e-234;
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Gapop 10.0 , Gapext 1.0
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Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	Sequence 21, Appl	Sequence 31, Appl	1, ,	-		Sequence 13629, A	Sequence 81, Appl	Sequence 7, Appli	Sequence 7, Appli	Sequence 7, Appli		Sequence 531, App	37,	Sequence 29, Appl	Sequence 79, Appl	2, A
		OI	US-09-249-011A-21	US-10-027-075-31	US-10-000-433-1	US-09-954-456-771	US-09-859-053-33	US-10-198-846-13629	US-09-800-729-81	US-09-992-600A-7	US-09-924-340-7	US-10-000-489-7	US-10-000-986-7	US-09-822-830A-531	US-09-859-053-37	US-09-859-053-29	US-09-800-729-79	US-09-799-514-2
		DB	11	15	15	11	11	15	10	12	12	15	15	11	11	11	10	70
		Length	1960	1708	3881	1244	948	1045	941	968	896	. 968	968	913	970	974	066	1033
ď	Query	ore Match Length DB II	100.0	55.7	53.3	30.4	26.7	26.7	26.7	26.7	26.7	26.7	26.7	26.7	26.4	26.4	26.4	26.4
		Score	1960	1091.2	1044	595.8	523.4	523.4	523	523	523	523	523	522.8	518.4	518.4	518.4	518.4
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Gaps 0.5

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Query Match
100.0%; Score 1960;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1960; Conservative 0; Mismatches

; FEATURE: ; NAME/KEY: CDS ; LOCATION: (768)..(1087) US-09-249-011A-21

TYPE: DNA
ORGANISM: Mus sp.
FEATURE:
NAME/KEY: CDS
LOCATION: (12)..(408)

LENGTH: 1960

DB 11; Length 1960; Indels

17 518.4 26.4 1230 15 US- 18 517.4 26.4 1184 15 US- 20 509.4 26.0 1775 15 US- 21 506.4 25.8 1202 15 US- 22 504.8 25.8 928 15 US- 23 504.8 25.8 928 15 US- 24 491.4 25.1 272 15 US- 25 646.4 23.9 853 15 US- 26 469.4 23.9 853 15 US- 27 465.8 23.6 477 11 US- 28 462 23.6 477 11 US- 30 462 23.6 477 11 US- 31 450.2 23.6 477 11 US- 33 435.4 22.4 829 15 US- 445.2 3.6 477 11 US- 34 439.4 22.4 829 15 US- 445.8 20.3 442 10 US- 35 424.4 21.7 19 US- 36 424.4 21.7 19 US- 37 416.8 21.3 520 11 US- 43 39.8 20.3 412 15 US- 44 392.8 20.0 394 15 US- 44 392.8 20.0 394 15 US- 44 392.8 20.0 396 11 US- 50-249-011A-21 50-249-01A-21 50-249-0	-158-646-59 Sequence 59, Appl -158-646-66 Sequence 60, Appl -158-646-64 Sequence 64, Appl -158-646-57 Sequence 57, Appl -158-646-55 Sequence 57, Appl -198-846-10845 Sequence 10845, Appl -158-646-68 Sequence 63, Appl -158-646-68 Sequence 68, Appl -198-846-14013 Sequence 68, Appl	864-761-4801 292-758-57 309-5678-14 158-646-65 198-846-13859 878-178-1407 846-935-1407 849-011A-7 198-846-13125 86quence 146-502-1407 86quence 146-502-1407 86quence 148-502-1407 86quence	1A NOGLOBULIN REACTIVE WITH B7-2 AND METHODS THEREWITH 249,011A
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  1130 AGAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCA 1189
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APPLICANT: ISHIGA, ISAGO
APPLICANT: Halk, Ed
APPLICANT: Halk, Ed
APPLICANT: Halk, Ed
APPLICANT: Halk, Ed
TITLE OF INVENTION: TRANSGENIC TRANSCHROMOSOMAL RODENTS FOR MAKING HUMAN
TITLE OF INVENTION: ANTIBODIES
FILE REFERENCE: 012110US
CURRENT APPLICATION NUMBER: US 60/250,340
PRIOR PLLING DATE: 2001-11-30
PRIOR PLLING DATE: 2000-11-30
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATCHIL Ver. 2.1
SEQ ID NO 11
                                                                                                    1190 GCCTGACCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7
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99.8%; Pred. No. 3.7e-255;
tive 0; Mismatches 0;
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Best Local Similarity 99.89
Matches 1066; Conservative
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                    COUNTRY: USA

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/10/027,075
FILING DATE: 20-Dec-2001
CLASSIFICATION SATA:
PRIOR APPLICATION ADATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 55.7%; Score 1091.2; DB 15; Lengt Best Local Similarity 99.6%; Pred. No. 2.1e-267; Matches 1115; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 09/227,595
FILING DATE: cUnknown>
ATORNEY/AEBNT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 35,207
REGISTRATION NUMBER: 35,207
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-10-027-075-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1708 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
STATE: Massachusetts
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S-09-954-456-771
Sequence 771, Application US/09954456
Patent NO US20020115057A1
GENERAL INFORMATION:
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Best Local Similarity 69.3%;
Matches 882; Conservative
                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
US-09-954-456-771
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Therapeutic Agents Using Cam 131 120 191 162 222 311 282 431 400 251 AAATTGTGT----TGACACAGTCTCCAGCCACCCTGTCTTTGTCTCCAGGGGAAAGAGCC 456 9 GACATTGTGCTGACACAGTCTCCAGATTCCCTGGCTGTAAGCTTAGGAGAGAGGGCCACT 132 ATTAGCTGCAAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAGAGAACTACTTGGCT 121 CTCTCCTGCAGGGCCAGTCAGAGTGT-------TGGCAGCTACTTAGCC TGGTACCAGCAGAAACCAGGGCAGCCTCCTAAACTGCTGATCTACTGGGCATCCACTAGG 163 TGGTACCAACAGAAACCTGGCCAGGCTCCCAGGCCCCTCATCTATGATGCATCCAACAGG GAATCTGGGGTCCCTGATCGCTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACC ATCAGCAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGCAGCCAATCTTATAATCTT 283 ATCAGCAGCCTAGAGCCTGAAGATTTTGCAGTTTATTACTGTCAACACGTGACAA--TT 372 TACACGTTCGGACAGGGGACCAAGGTGGAAATAAAACGTAAGTAGTCTTCTCAACTTAG 341 GGCCTCCGGGGGCCACTTTCGGCGGAGGGACCAAGGTGGAGATCAAACATACCACCGGAG AAAŢTCTAAACTCTGAGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTT 12 ATGGATTCACAGGCCCAGGTTCTTATATTGCTGCTATGGGTATCTGGCACCTGTGGG GAPPLICANTY: Young, Paul
TITLE OF INVENTION:
TITLE OF INVENTION: Sets
TITLE OF INVENTION: Sets
FILE REFERENCE: 69290-76
CURRENT FILING DATE: 2001-09-18
PRIOR PAPLICATION NUMBER: US/60/234,617
PRIOR APPLICATION NUMBER: US/60/234,052
PRIOR APPLICATION NUMBER: US/60/234,052
PRIOR APPLICATION NUMBER: US/60/234,923
PRIOR APPLICATION NUMBER: US/60/234,923
PRIOR FILING DATE: 2000-09-26
PRIOR FILING DATE: 2000-09-25
PRIOR PILING DATE: 2000-09-26
PRIOR FILING DATE: 2000-09-26
PRIOR FILING DATE: 2000-09-26
PRIOR PILING DATE: 2000-09-26
PRIOR PILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,711
PRIOR PILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27 Score 595.8; DB 11 Pred. No. 2.8e-141; 0; Mismatches 362;

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LOCATION: (1)...(27)
NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                  NAME/KEY: 5'UTR
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Patent No. US20020102658A1
GENERAL INFORMATION:
APPLICANT: Tezuka, Katsunari
APPLICANT: Tezuka, Katsunari
APPLICANT: Tezuka, Katsunari
APPLICANT: Hori, No. US20020102658A1uaki
APPLICANTION: HORMACEUTICAL USE THEREOF
TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
FILE REFERENCE: 06501-079001
CURRENT APPLICATION NUMBER: US 2001-05-16
PRIOR APPLICATION NUMBER: UP 2001-99508
                                                                                                                612 TITIAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCT
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492 TACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAA
                                                         552 ACAATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAACTCAAAACATCAAGA
                                                                                    517 céregeceásecreceásececerententanicarecaacaacaceácrasearecea
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Pred. No. 6.7e-123;
0; Mismatches 2;
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: JP 2000-147116
PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 33
LENGTH: 948
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US-10-198-846-13629
; Sequence 13629, Application US/10198846
; Publication No. US20030099974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (1)...(948)
OTHER INFORMATION: n = A,T,C or G
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99.6%;
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NAME/KEY: 3 'UTR
LOCATION: (739) ... (948)
NAME/KEY: sig_peptide
LOCATION: (28) ... (87)
NAME/KEY: misc_feature
LOCATION: (10) ... (948)
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ORGANISM: Homo sapiens
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TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND FILE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049 WINDER: US/10/198,846
CURRENT PELICATION NUMBER: US/10/198,846
PRIOR APPLICATION NUMBER: 05/306,220
PRIOR APPLICATION NUMBER: 60/306,220
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: FASISEQ for Windows Version 4.0
LENGTH.: 1045
                                                                                                                                                                                                                                                                                               Length 1045;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 81, Application US/09800729
Farent No. US20020068319A1
GENERAL INFORMATION:
JAPLICANT: Ni et al.
FILLE OF INVENTION: 32 Human secreted proteins
FILLE PEPERANCE: PZ044P1
CURRENT APPLICATION NUMBER: US/09/800,729
CURRENT FILING DATE: 2001-03-08
FRIOR APPLICATION NUMBER: PCIY/US00/26013
FRIOR APPLICATION NUMBER: 60/155,709
FRIOR FILING DATE: 1999-09-24
                                                                                                                                                                                                                     TYPE: DNA
CRGANISM: Homo sapiens
US-10-198-846-13629
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US-09-800-729-81
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821 GGTCCTCCAGCTCATTCTTTCACCTCACCCCCTCCTCCTCGCTTTAATTATGCTAA 880
821 GGTCCTCCAGCTCATCTTTCACCTTCACCCCCCTCCTCCTCCTCTTTAATTATGCTAA 880
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Best Local Similarity 100.0%; Pred. No. 8.4e-123;
Matches 523; Conservative 0; Mismatches 0;
; SEQ ID NO 81
; LENGTH: 941
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-800-729-81
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US-09-992-600A-7
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60/298,698
                   60/302,277
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/
PRIOR PAPLICATION NUMBER: US 60/
PRIOR APPLICATION NUMBER: US 60/
PRIOR APPLICATION NUMBER: US 60/
PRIOR APPLICATION UNMBER: US 60/
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-05-25
SOFTWARE: JPatent
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
26.7%;
Best Local Similarity 100.0%;
Matches 523; Conservative 0
                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                   LOCATION: 928.933
NAME/KEY: polyA site
LOCATION: 953.968
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NAME/KEY: CDS
LOCATION: 32..748
NAME/KEY: 3'UTR
LOCATION: 749..968
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NAME/KEY: 5'UTR
LOCATION: 1..31
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Publication No. US20030027248A1
GENERAL INFORMATION:
APPLICANT: Bejanin, Stephane
APPLICANT: Tanaa, Hiroaki
TITLE OF INVENTION: HUWAN CDNAS AND PROTEINS AND USES THEREOF
FILE REPERENCE: 91.US2.REG
CURRENT APPLICATION UNUBER: US/09/924,340
CURRENT FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: US 60/305,456
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100.0%; Pred. No. 8.5
:ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.1
Matches 523; Conservative
                                                                                                                                                                                                FEATURE:

NAME/KEY: polyA signal
LOCATION: 928..933
FEATURE:
NAME/KEY: polyA site
LOCATION: 933..968
US-09-992-600A-7
                 TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                     749..968
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                                                                              LOCATION:
FEATURE:
NAME/KEY:
LOCATION:
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NAME/KEY:
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                                                                                                  768 GAACTGTGGCTGCACCATCTTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTG
                                                                                                                                                   429 GAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTG
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                                                      Gaps
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                                                   Indels
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Pred. No. 8.5e-123;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-000-489-7; Sequence 7; Application US/10000489; Publication No. US20030092011A1; GENERAL INFORMATION:
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948 GCAAGGACACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGA 1007
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                                                                                                                                               US-10-000-986-7, Application US/10000986

Publication No. US20030096247A1

GENERAL IMPORMATION:

APPLICANT: Benjanin, Stephane

APPLICANT: Benjanin, Stephane

APPLICANT: Tanaka, Hixoaki

TITLE OF INVENTION: HUWAN CDNAS AND PROTEINS AND USES THEREOF

FILE REFERENCE:

CURRENT APPLICATION NUMBER: US/10/000,986

CURRENT FILING DATE: 2001-11-4

PRIOR PELLOR DATE: 2001-08-06

PRIOR APPLICATION NUMBER: PCT/1B01/01715

PRIOR APPLICATION NUMBER: PCT/1B01/01715

PRIOR APPLICATION NUMBER: US 60/305,456

PRIOR APPLICATION NUMBER: US 60/305,277

PRIOR PELLING DATE: 2001-06-29

PRIOR FILING DATE: 2001-06-29

PRIOR FILING DATE: 2001-06-29

PRIOR FILING DATE: 2001-06-29

PRIOR FILING DATE: 2001-06-25

NUMBER OF SEQ ID NOS: 112

SEQ ID NO 7

LENGTH: 968
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        909 IGTIGGAGGAGAATGAATAAATAAAGTGAATCTTIGCACCTGT 951
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Best Local Similarity 100.0%; Pred. No. 8.5e-123;
Matches 523; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | NAME/KEY: 5'UTR
| LOCATION: 1.31
| NAME/KEY: CDS
| LOCATION: 32.748
| NAME/KEY: 79.968
| NAME/KEY: POLYA signal
| LOCATION: 749.968
| NAME/KEY: POLYA signal
| LOCATION: 928.93.3
| LOCATION: 953.968
| US-10-000-986.7
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ORGANISM: Homo sapiens
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HITLE OF INVENTION: HITCARI

FILER REFERENCE: 91.026.DIV

CURRENT APPLICATION: HUMAN CDNAS AND PROTEINS AND USES THEREOF

FILER REFERENCE: 91.026.DIV

CURRENT APPLICATION NUMBER: US/10/000,489

CURRENT PILING DATE: 2001-11-14

PRIOR PILING DATE: 2001-10-8-06

PRIOR FILING DATE: 2001-08-06

PRIOR PAPLICATION NUMBER: US 60/302,277

PRIOR PAPLICATION NUMBER: US 60/298,698

PRIOR PAPLICATION NUMBER: US 60/298,698

PRIOR APPLICATION NUMBER: US 60/298,598

PRIOR PAPLICATION NUMBER: US 60/293,574

PRIOR PILING DATE: 2001-06-25

NUMBER OF SEQ ID NOS: 112

SEQ ID NO 7

LENGTH: 968
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
CRGANISM: Homo sapiens
FRATURE:
NAME/KEY: 5'UTR
LOCATION: 1..31
NAME/KEY: 5'UTR
LOCATION: 32..748
NAME/KEY: 3'UTR
LOCATION: 749..968
NAME/KEY: polyA_signal
LOCATION: 928..933
NAME/KEY: polyA_signal
LOCATION: 928..933
NAME/KEY: polyA_signal
LOCATION: 928..933
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: TSUJI, TAKASHI
APPLICANT: TSUJI, TAKASHI
APPLICANT: TSUJI, TAKASHI
TITLE CANTIN: HOUND MONOCLONAL ANTIBODY AGAINST A
TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
FILE REFERENCE: 06501-079001
CURRENT APPLICATION NUMBER: US/09/859,053
CURRENT PILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: JP 2001-99508
PRIOR FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: JP 2000-147116
PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 37
LENGHH: 970
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     1186 GCGGTCCTCCAGCTCATCTTTCACCTCACCCCCTCCTCCTTGGCTTTAATTATGCT
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Pred. No. 1.3e-121;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                              ; Sequence 37, Application US/09859053; Patent No. US20020102658A1; GENERAL INFORMATION:
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26.4%;
Best Local Similarity 99.8%;
Matches 519; Conservative
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| LOCATION: (1)...(32)
| MAME/KEY: CDS
| LOCATION: (33)...(740)
| NAME/KEY: 3.UTR
| LOCATION: (744)...(970)
| NAME/KEY: sig_peptide
| LOCATION: (33)...(92)
| US-09-859-053-37
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                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 531, Application US/09822830A
Patent No. USJ0020142952A1
GENERAL INFORMATION:
APPLICANT: Genetics Institute, Inc.
APPLICANT: Genetics Institute, Inc.
APPLICANT: Genetics Institute, Inc.
APPLICANT: Fechtel, Kim
APPLICANT: Fechtel, Kim
APPLICANT: Fechtel, Kim
APPLICANT: Galukota, Kachard J.
APPLICANT: Galukota, Kachard J.
APPLICANT: Galukota, Kamalakar
APPLICANT: Galukota, Sacora Marana APPLICATION NUMBER: GO/195,604
PRIOR APPLICATION NUMBER: GO/195,604
PRIOR APPLICATION NUMBER: GO/195,604
PRIOR FILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 631
LENGTH: 913
1128 TGACCCCCTCCCATCCTTTGGCCTCTGACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA; ORGANISM: Homo sapiens
US-09-822-830A-531
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	RESULT 15 US-09-800-729-79 US-09-800-729-79 Sequence 79, Application US/09800729 Sequence 79, Application US/09800729 Sequence 79, Application US/09800729 SERENT NO. US20020068319A1 SPECIAL INFORMATION: A TITLE OF INVENTION: 32 Human secreted proteins FILE REFERENCE: PZ04491 CURRENT FILING DATE: 2001-03-08 SPIOR APPLICATION NUMBER: US/09/800,729 CURRENT FILING DATE: 2001-03-08 SPIOR PILING DATE: 2000-09-24 SPIOR PILING DATE: 1999-09-24 NUMBER OF SEQ ID NOS: 217 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 79 LENGTH: 990 TYPE: DNA CRGANISM: Homo sapiens SPATURE: SPATURE: SPATURE: SPATURE: NAME/KEY: SITE	FORMATION: n equals a,t,g, or c 9-79 h Similarity 99.8%; Pred; No. 1.3e-121; 19; Conservative 0; Mismatches 1; Indels 0; Gaps 6 AGGARCTOGGCGCGCGCTCTCATCTCTCGCCCATCTGATGAAATC 6 [[[[[[[[[[[[[[[[[[[[[[[[[[[[[[[[[[[[U 4-4 4-	508 946 568 1006	
Oy 1126 CCTGACCCCTCCCATCCTTGGCCTCTGACCCTTTTCCACAGGGGACCTACCCCTATT 1185 Db 779 CCTGACCCCTCCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCCTATT 818 Oy 1186 GCGGTCCTCCAGCTCTTTCACCTCCTCCTCTCTCTTTGGCTTTAATTATTATTTT 838 Oy 1246 AATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCA 1285 Db 899 AATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCA 1285 BB 899 AATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCA 938 RESULT 14	US-09-89-053-29 US-09-889-053-29 Patent No. US20020102658A1 Fatent No. US20020102658A1 Fatent No. US20020102658A1 Fatent No. US20020102658A1 FAPLICANT: Teaula, Kateunari APPLICANT: Teaula, Kateunari APPLICANT: Teaula, Kateunari APPLICANT: Teaula, Kateunari APPLICANT: Hori, No. US20020102658A1uaki APPLICANT: Hori, No. US20020102658A1uaki APPLICANT: HORIN WONOCLONAL ANTIBODY AGAINST A TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE ALLIM AND TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF TITLE OF INVENTION: 05-05-05-06 FRIOR PAPLICATION NUMBER: US/09/859,053 FRIOR APPLICATION NUMBER: UP 2001-09-06 FRIOR FILING DATE: 2001-03-08 FRIOR PELLING DATE: 2000-05-18 NUMBER OF SEO ID NOS: 43 SEO ID NO 29 IENGTH: 974 TYPE: DNA CORGANIEM: HOMO SapienS	NAME/KEY: S'UTR NAME/KEY: S'UTR NAME/KEY: CDS NAME/KEY: CDS NAME/KEY: CDS NAME/KEY: CDS NAME/KEY: 3'UTR NAME/KEY: 3'UTR NAME/KEY: 4'GP4) NAME/KEY: 4'GP40 NAME/KEY: 4'GP60 NAME/KEY: 4'GP60	Ouery Match 26.4%; Score 518.4; DB 11; Length 974; Best Local Similarity 99.8%; Pred. No. 1.3e-12; Matches 519; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Qy 766 AGGAACTGGTGCTCTCTCTCTCTCCGCCATCTGATGAGGATTGAAATC 825 Db 425. ACGAACTGTGGCTGCACCATCTTCATCTTCCGCCATCTGATGAGGAGTTGAAATC 826		Oy 946 CAGCAAGGACCTACAGCCTCAGCACCCTGACCAGCAAGCA

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Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-353-400-24 PCT-US95-11405-34 US-08-487-283A-15 US-08-487-283A-13 US-08-487-283A-14 US-09-097-309-5 US-09-097-309-5 US-09-460-587-5 US-09-460-587-5 US-08-463-587A-2 US-08-463-587A-2 US-08-923-854-24 PCT-US91-09133-25 US-08-923-854-24 PCT-US91-09133-25 US-09-607-756-1 US-08-286-740-4 PCT-US95-09576-4 US-08-286-740-4	ALIGNMENTS 247352 .A. B. CS AGAINST HUMAN CD40 E 09/026,291 -19 -19	Score 1611.8; DB 4; Pred. No. 0; 0; Mismatches 137; I CAGGTTCTATATATGCTGCTGCTA CAGCTTCTCTTCCTCGTGCTACTC CAGTCTCCAGATTCCTGGTGTA CAGTCTCCAGATTCCTGGTGTA CAGTCTCCAGATTCCTGGTGTA CAGTCTCCAGGTGTA CAGTCTCCAGGTGTA CAGTCTCCAGGTGTA CAGTCTGCAGGTGTA CAGTCTGCAGGTGTA CAGTCTGCAGGTGTA CAGTCTGTA CAGTCTA CAGTCTGTA CAGTCTA C
74.6 17.1 1940 1 13.4 16.6 17.1 1940 1 13.3 4 16.5 726 4 16.5 726 4 16.5 726 4 16.4 2143 3 16.4 2143 4 16.4 2143 4 16.4 2178 1 16.4 2178 1 16.4 2178 3 16.4 2178 3 16.4 2178 3 16.4 2178 3 16.4 2178 3 16.4 2178 1 16.4 2178 3 16.4 2178 1 16.4 2178 3 16.4 2178 1 16.4 2178 3 16.4 2178 1 16.4 2178 5 16.4 2178 5 16.4 16.4 7305 1	Application US/09 6315693 ORMATION: Arutfo, Alejandro Siadak, Anthony W Berry, Karen K. Harris, Linda Thorne, Barbara A Bajorath, Jurgen Wu, Herren Wu, Herren Wu, Herren Wu, ELCATION: ENCE: DB2a SEQUENC	
. 9001244444444444444444444444444444444444	RESULT 1 US-09-247-352-6 Sequence 6, App Patent No. 6312. GENERAL INFORMA APPLICANT: Sia APPLICANT: BET APPLICANT: BET APPLICANT: BET APPLICANT: HOW, APPLICANT: HOW, APPLICANT: HOW, APPLICANT: WAL, APPLICAN	Quer Matc

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189 GCTTGGTACCAGCAGAAACCAGGGCAGCCTCCTAAACTGCTGATCTACTGGGCATCCACT

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119	RESULT 3 US-07-916-098A-54 US-07-916-098A-54 Sequence 54, Application US/07916098A Sequence 54, Application US/07916098A Sequence 54, Application US/07916098A Sequence 54, Application US/07916098A SEPLICANT: BURKLY, LINDA C. APPLICANT: HUMAS, DAVID M. APPLICANT: ROSA, WARGARET D. APPLICANT: ROSA, WARGARET D. APPLICANT: ROSA, USEFH J. APPLICANT: ROSA, USE
9 GGGGGCATTGTGCTGCACACACTCCTGCCTCACACTCACACACTCACACACA	6 4 4 4 4 4 4

us-09-627-896b-21.rni

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        1450
        CCTCCCTCAAACCCACAAGCCTTCTGTCCTCACAGTCCCCTGGGCCATGGTAGGAGGAC
        1509

        1450
        CCTCCCTCAAACCCATCTGTCCTCACAGTCCCCTGGGCCGTGGTAGGAGAGAC
        1523

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1330 TTTTACCAACTACTCCAATTTCTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCA 1389
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1285 AAGTGAATCTTTGCACCTGTGGTTTCTCTCTTTCCTCAATTTAATAATTATTATCTGTTG
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                                                                                                                                                                           AACAATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAGAAACTTCAAAACATCAAG
                                                                                                                                                                                                                                                                                                 685 TGTCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1701;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 72.9%; Score 1429.4; DB 2; Length Best Local Similarity 93.1%; Pred. No. 0; Matches 1534; Conservative 0; Mismatches 96; Indels
STATE: ILLINOIS

COUNTRY: U.S.A.

ZIP 66060

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: BM PC COMPATIBLE
COMPUTER: BM PC COMPATIBLE
COMPUTER: BM PC COMPATIBLE
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/916,098A
FILING DATE: JULY 24, 1992
CLASSIFICATION NUMBER: PCT/US91/08843
FILING DATE: NO. 5871732ember 27, 1991
CLASSIFICATION '0 S817732ember 27, 1991
CLASSIFICATION '0 S817732ember 27, 1991
CLASSIFICATION NUMBER: OS 6949
REFERENCE/COCKET NUMBER: 26,949
REFERENCE/COCKET NUMBER: 92,310-G
TELEFAX: (312) 715-1234
TELECOMMUNICATION INFORMATION:
TELEFAX: (312) 715-1234
TELECOMMUNICATION INFORMATION:
TELEFAX: (312) 715-1234
TELEFAX: (312) 715-1234
TELEFAX: (312) 715-1234
TELEX: 910/221-5317
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 1701 Dass pairs
TYPE: NOLOGY: linear
MODECUE TYPE: DNA (Genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) OTHER INFORMATION: /note= "pMDR1006 insert" US-07-916-098A-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         311 CATCAGCAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGCAGCCAATCTTATAATCT 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    340 CATCAGCAGTTTGCAGGCTGAAGACGTGGCAGTTTATTACTGTCAGCAATATTATGCTA 399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72.9%; Score 1429.4; DB 2; Length 1701; 93.1%; Pred. No. 0; tive 0; Mismatches 96; Indels 17;
                                                                                                                                                                   /note= "pMDR1007 insert: pre-5A8 humanized light chain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 93.1<sup>3</sup>
Matches 1534; Conservative
                                                                                                           misc_feature
                                    LOCATION: 438.781
FRATURE:
NAME/KEY: misc_featu
LOCATION: 1
OTHER INFORMATION: /
OTHER INFORMATION: /
FRATURE:
NAME/KEY: exon
LOCATION: 35.436
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NAME/KEY: exon
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782..1101
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438..781
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; LOCATION:
US-07-916-098A-55
                NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 55, Application US/07916098A

Patent No. 581732

GENERAL INFORMATION:
APPLICANT: BURKLY, LINDA C.
APPLICANT: CHISHOLM, PATRICIA L.
APPLICANT: THOMAS, DAVID W.
APPLICANT: THOMAS, DAVID W.
APPLICANT: ROSA, MASCARET D.
APPLICANT: ROSA, MATICOPET D.
APPLICANT: ROSA, MATICOPET
                                                                                                                                                                          1584 CTTACGGTCATATATCCTTTGATTCCATGGGAATCAACCAAGGCAAATTTTTCAA 1643
1510 ITGCTTCCTTGTTTTCCCCTCCTCAGCCAAGCCCTCATAGTCCTTTTTAAGGGTGACAGGT
                                              1524 TIGCTICCTIGTTTTCCCCTCCTCAGCAAGCCCTCATAGTCCTTTTTAAGGGTGACAGGT
                                                                                                                                     CTTACAGTCATATATCCTTTGATTCAATTCCCTGGGAATCAACCAAAGCAAATTTTTCAA
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PT/US91/08843

FILING DATE: No. 5871732ember 27, 1991
CLASSIFTCATION: 424
APPLICATION NUMBER: 07/618,542
FILING DATE: No. 5871732ember 27, 1990
CLASSIFTCATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: JOHN J. MC DONNELL
RAGGISTRATION NUMBER: 26,949
PREGISTRATION NUMBER: 26,949
PREGISTRATION NUMBER: 26,949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESTONDENCE ACLEGRETT & WITCOFF, LTD.
STREET: 10 SOUTH WACKER DRIVE
CITY: CHICAGO
STATE: LLLINOIS
COUNTRY: U.S.A.
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/916,098A
FILING DATE: JULY 24, 1992
                                                                                                                                                                                                                                                                                                                                 1644 AAGAAGAAACCTGCGGCCGATCGATTC 1670
                                                                                                                                                                                                                                                                 AAGAAGAAACCTGCTATAAAGAGAATC 1656
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join(101..437, 782..1101)
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 715-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (312) 715-1234
TELEX: 910/221-2317
INPORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1701 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 4
US-07-916-098A-55
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                                                                                                                                                                                                                                                                           985 AGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAA 1044
                                                                                                                                                                                                                                                                                                                                                     AGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCC 1150
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  TTCATCTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTG 850
                                                                                 CTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAA 910
                                                                                                         TCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTC 970
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8147 ACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAAGAGCTCCAACAAAA
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ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
CITY: MAJ
COUNTRY: USA
ZIP: 0273
COMPUTER READABLE FORM:
MEDIUM TRYE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TRYE: Floppy disk
COMPUTER: TAPE: TAPE
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LOCATION: 1.1399
OTHER INFORMATION: /note= "Function = "Expression
OTHER INFORMATION: Vector Coding Sequence""
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P. C.

& Reynolds,

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ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,246A
FILING DATE: 04-MAY-1994
CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Wagner, Richard W.
REGISTRATION NUMBER: 34,480
REFERENCE/DOCKET NUMBER: 34,480
REFERENCE/DOCKET NUMBER: 34,480
REPERENCE/DOCKET NUMBER: 34,480
REPERENCE/DOCKET NUMBER: 34,480
REPERENCE/DOCKET NUMBER: 34,480
TELEPAN: (617) 861-6240
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 13999 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                              FILING DATE: 04-MAY-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/800,458
FILING DATE: 26-NOV-1991
PRIOR APPLICATION NUMBER: PCT/US90/05077
FILING DATE: 07-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/404,089
TITLE OF INVENTION: ANTIBODY-NEUROPH
TITLE OF INVENTION: CONJUGATES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith
STREET: Two Militia Drive
                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= Vector (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60.4%;
ilarity 99.5%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 07-SEP-1989 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: 1..13999
OTHER INFORMATION: /not
OTHER INFORMATION: Vect
                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                           STREET: Two Mili-
CITY: Lexington
STATE: MA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity
Matches 1208; Conserv
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FEATURE:
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                                     GAATAACTICTATCCCAGAGAGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATC
                                                                                                                                                                                                                        GGGTAACTCCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAAGGACCTACAGCCTCAG
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                                                                                             CATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTTGTGTCCCTGCT
                                                                                                                                       GAATAACTTCTATCCCAGAGGCCCAAAGTACAGTGGAAGGTGGATAAACGCCCTCCAATC
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"Function = "Expression
Coding Sequence""
                                                                            DB 4;
                                                                          Score 1184.2; DB 4. Pred. No. 2.1e-298; 0; Mismatches 4;
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US-08-222-246A-24
; Sequence 24, Application US/08232246A
; Patent No. 6329508
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC

```
APPLICANT: CHISHOLM, PATRICIA L.
APPLICANT: THOMAS, DANID W.
APPLICANT: ROSA, MARGARED J.
APPLICANT: ROSA, MARGARED J.
APPLICANT: ROSA, JOSEPH J.
ADDRESSER: ALLEGRETH: WITCOFF, LTD.
CORRESPONDER BARGESS:
ADDRESSER: ALLEGRETH: WITCOFF, LTD.
CITY: CHICAGO
CITY: CHICAGO
CITY: CHICAGO
CITY: CHICAGO
CONVEY: U.S.A.
ADDRESSER: ALLEGRETH: PC-DOS/MS-DOS
CONVEY: U.S.A.
ADDRESSER: ALLEGRETH: AND TASA
CONVEY: U.S.A.
ADDRESSER: ALLEGRETH: AND TASA
CONVEY: U.S.A.
ADDRESSER: ALLEGRETH: AND TASA
CONVEY: U.S.A.
ADDRESSER: AND HITCORD AND TASA
CONVEY: U.S.A.
APPLICATION NUMBER: USCO/1916,098A
FILING ONLY WREN: USCO/1916,098A
FREEERNEY CONCRETTION WRENE: USCO/1916,098A
FREEERNEY CONCRETTION WRENE: USCO/1916,098A
FREEERNEY CONCRETTION WRENE: USCO/1916,098A
FREEDRING CHARACTERISTICS:
FREEERNEY CONCRETTION WRENE: USCO/1916,098A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: 1
OTHER INFORMATION: /note= "pMDR986 insert"
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              3327 TCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACCCCAAGGGCAGAACTTTGT 8386
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S-07-916-098A-53 Sequence 53, Application US/07916098A Patent No. 2871732 GENERAL INFORMATION: APPLICANT: BURKLY, LINDA C.

```
APPLICANT: BURKLY, LINDA C.

APPLICANT: CHISHOLM, PATRICIA L.

APPLICANT: THOWAS, DAVID W.

APPLICANT: ROSA, WARGARET D.

APPLICANT: ROSA, WARGARET J.

APPLICANT: ROSA, JOSEPH J.

TITLE OF INVENTION: ANTI-CD4 ANTIBODY, HOMOLOGS USEFUL IN

TITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION

NUMBER OF SEQUENCES: 61

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 TICIAAACICIGAGGGGICGGATGACGIGGCCATICITIGCCIAAAGCATIGAGITIAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LOCATION: 1 _ OCHER INFORMATION: /note= "pSAB153 insert" US-0-916-0984-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRICE APPLICATION 1213.

APPLICATION NUMBER: PCT/US91/08843
FILING DATE: No. 5871732ember 27, 199
CLASSIFICATION NUMBER: 07/618,542
FILING DATE: No. 5871732ember 27, 199
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: JOHN J. MC DONNELL
REGISTRATION:NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 92,310-G
TELECOMMUNICATION: INFORMATION:
TELEPHONE: (312) 715-1000
                                                                                                                                                                                        E: ALLEGRETTI & WITCOFF, LTD
10 SOUTH WACKER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/916,098A
FILING DATE: July 24, 1992
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                E: Floppy disk
IBM PC compatible
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(312) 715-1234
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Best Local Similarity 99.6%;
Matches 1205; Conservative
                                                                                                                                                                                                                                                                                                                                                                                        WORD PERFECT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 910/221-5317
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid
                                                                                                                                                                                                                                                                                    ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                  STATE: ILLINOIS COUNTRY: U.S.A.
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                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                    COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE:
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                        264 TGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCCAAGGGCAGAACTTTGTTA
                                                                                                              324 CTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTTCA
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TGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACCCCAAGGGCCAGAACTTTGTTA
                                                                          CTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTTCA
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RESULT 8 US-07-916-098A-51 Sequence 51, Application US/07916098A ; Patent No. 5871732

143

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Gaps

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203 674

615 TAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCTGTC

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Sequence 31, Application US/09227595
Patent No. 644479
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICAMY: Gray, Gary S. et al.
TITLE OF INVENTION: CTLA4-Immunoglobulin Fusion Proteins
TITLE OF INVENTION: Having Modified Effector Functions and Uses Therefor NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            650 GCTAGGAAGAACTCAAAACATCAAGATTTTAAATACGCTTCTTGGTCTCCTTGCTATAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Version #1.25
                                                                                                                                                                                                                                                                                                                       ZIP: 02109-1875
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/227,595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILTING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLIC
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Best Local Similarity 99.6%;
Matches 1115; Conservative (
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US-09-227-595-31
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564 GCACCCTGAGGCAAGCAGAGAACACAAACACAAAGTCTAGGCCTGGGAAGTCA 623
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                                                                                                                                                                                         CTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTTCA 383
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              TAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCTGTC 263
                                                                                                                                                       CITAAACACCAICCIGIIIGCIICIIICCICAGGAACIGIGGCIGCACCAICIGICIICA 794
                                                                                                                                                                                                                                                         TCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGA 854
                                                             TGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACCACCCCAAGGGCAGAACTTTGTTA
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RESULT 9 US-09-227-595-31

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433 AATTCTAAACTCTGAGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTT
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Pred. No. 3.8e-262;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-0CT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US96/16433
FILING DATE: 10-0CT-1996
PRIOR APPLICATION NUMBER: US 08/758,417
FILING DATE: 02-DEC-1996
PRIOR APPLICATION NUMBER: US 08/758,417
FILING DATE: 01-DEC-1996
PRIOR APPLICATION NUMBER: WO PCT/US97/21803
FILING DATE: 01-DEC-1997
ATMORIEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 014643-009040US TELECOMMUNICATION INFORMATION:
                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/904,068
                                                                                                                                                                                                                                         PELLOATION NUMBER: US 07/904,068
FILING DATE: 23-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/096,762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 03-DEC-1993
REIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
PRIOR APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/352,322
APPLICATION NUMBER: US 08/352,322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 22-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION TO APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/155,301 FILING DATE: 18-NOV-1993 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/161,739 FILING DATE: 03-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/352,322 FILING DATE: 07-DEC-1994 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/544,404 FILING DATE: 10-OCT-1995 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36,429
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TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 365
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53.3%;
99.8%;
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Best Local Similarity 99.8'
Matches 1066; Conservative
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     FILING DATE: 13
CLASSIFICATION:
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945 ACAGCAAGGACAGCACCTACAGCTCAGCAGCACCCTGACGCAGACAAAGCAGACTACG
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BATELIN NO. 62525458

GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 421
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1604 GGAATCAACCAAAGCAAATTTTTCAAAAGAAGAAACCTGC 1643
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COMPUTER READABLE FORM;

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
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Center, Eighth Floor
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STREET: Two Embarcadero Ce
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-042-353-369
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433 AATTCTAAACTCTGAGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTT
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                                                                                           for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .,
Sequence 217, Application US/08758417A
Patent No. 6300129
GENERAL INPORMATION:
GENERAL LONDERGY, Nils
RAY, Robert M.
TITLE OF INVENTION: Producing Heterologous Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 3881;
                                                                                                                                                                                                                                 COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/08/758,417A
FILING DATE: 02-Dec-1996
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1995
APPLICATION NUMBER: US 08/32,322
FILING DATE: 10-OCT-1995
APPLICATION NUMBER: US 08/32,322
FILING DATE: 09-DEC-1994
APPLICATION NUMBER: US 08/16,699
FILING DATE: 09-DEC-1993
APPLICATION NUMBER: US 08/16,699
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/16,699
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/16,699
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/16,739
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/16,739
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/05,762
FILING DATE: 22-JUL-1993
APPLICATION NUMBER: US 08/05,762
FILING DATE: 22-JUL-1993
APPLICATION NUMBER: US 08/05,3131
FILING DATE: 22-JUL-1993
APPLICATION NUMBER: US 08/05,3131
FILING DATE: 16-DEC-1992
ATTORNEY/AGENT INFORMATION:
TELEPRANEY: (415) 576-0200
TELECOMMUNICATION INFORMATION:
TELEPRANEY: (415) 576-0300
INFORMATION FOR END ID NO: 217:
SEQUENCE CHARACTERISTICS:
LENGTH: 3081 Dasse pairs
TVDEST TOTAL AGE PAIRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                          NUMBER OF SEQUENCES: 417
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STRIE: Callifornia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53.3%; Score 1044; DB 4;
99.8%; Pred. No. 3.8e-262;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear SEQ ID NO: 217: US-08-758-417A-217
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 99.8
Matches 1066; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                         2674
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    2555 AATTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTT 2614
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                                      ACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAAAGGCTCCAACAAAA
                                                                                                           CAATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAACTCAAAACATCAAGAT
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Transgenic No. 6255458-Human Animals for
Producing Heterologous Antibodies
421
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APPLICATION NUMBER: US/09/042,353
  TITLE OF INVENTION: Transgenic No. 6255458-Humar TITLE OF INVENTION: Producing Heterologous Antit NUMBER OF SEQUENCES: 421
CORRESPONDENCE ADDRESS: ADDRESSE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US96/16433
FILING DATE: 10-OCT-1996
PRIOR APPLICATION NUMBER: WO PCT/US96/16433
FILING DATE: 10-OCT-1996
PRIOR APPLICATION NUMBER: US 08/758,417
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FILING DATE: 02-DEC-1996
FILING DATE: 02-DEC-1996
APPLICATION NUMBER: WO PCT/US97/21803
FILING DATE: 01-DEC-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 800
PRIOR APPLICATION BATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
PRIOR APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/853,408
APPLICATION NUMBER: US 07/904,068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
PRICOR APPLICATION DATA:
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
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PRIOR APPLICATION DATA:
APPLICATION
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/096 7/7
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 07/990,860 FILING DATE: 16-DEC-1992 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/053,131
                                                                                                                                                                                                                                                                                                                                                              UMBER: US/09/042,353
                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                          94111-3834
                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                          COUNTRY:
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REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 014643-009040US
TELECOMMUNICATION INPORMATION:
TELEPHONE: (415) 576-0200

Sequence 393, Application US/09042353 Patent No. 6255458 GENERL INFORMATION: APPLICANT: Lonberg, Nils APPLICANT: Kay, Robert M.

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                                                                                                                                                                                                  Length 3819;
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                                                                                                                                                                                       Ouery Match 36.2%; Score 709.4; DB 4; Best Local Similarity 99.6%; Pred. No. 4.9e-175; Matches 732; Conservative 0; Mismatches 1;
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US-08-758-417A-243
; Sequencë 243, Application US/08758417A
; Patent No. 6300129
; GENERAL INFORMATION:
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TELEFAX: (415) 576-0300
INFORMATION FOR EGO ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 3819 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                    ; TOPOLOGY: linear; MOLECULE TYPE: DNAUS-09-042-353-393
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Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
Producing Heterologous Antibodies
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                                                                                                                                                                                                                                                                                                           COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: DATE: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
PLING DATE: US-Dec-1996
CLASSIFICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
FILING DATE: 10-OCT-1996
APPLICATION NUMBER: US 08/32,322
APPLICATION NUMBER: US 08/32,322
APPLICATION NUMBER: US 08/32,322
APPLICATION NUMBER: US 08/35,322
APPLICATION NUMBER: US 08/35,323
APPLICATION NUMBER: US 08/35,332
APPLICATION NUMBER: US 08/15,739
APPLICATION NUMBER: US 08/15,739
APPLICATION NUMBER: US 08/15,301
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/15,301
FILING DATE: 12-OU-193
APPLICATION NUMBER: US 08/15,311
FILING DATE: 26-APP-193
APPLICATION NUMBER: US 08/05,762
APPLICATION NUMBER: US 08/05,762
APPLICATION NUMBER: US 08/05,762
APPLICATION NUMBER: US 08/05,762
APPLICATION NUMBER: US 08/05,763
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                                                                                                                     CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
CITY: California
COUNTRY: USA
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REGISTRATION NUMBER: 41,303
REFERENCE/DOCKET NUMBER: 014643-009030US
TELECOMMUNICATION INFORMATION:
TELEBHOKE: (415) 576-0200
TELEFAX: (415) 576-0300
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Pred. No. 4.9e-175;
0; Mismatches 1;
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Best Local Similarity 99.6%;
Matches 732; Conservative (
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INFORMATION FOR SEQ ID NO:
                                                                                                     NUMBER OF SEQUENCES:
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2088 GAACTTTGTTACTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACC 2147
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                                                     GTGGGGACATTGTGCTGACACACTCTCCAGATTCCCTGGCTGTAAGCTTAGGAGAGAGGGG
                                                                                                          CCACTATTAGCTGCAAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAGAGAACTACT
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CCACCATGGATTCACAGGCCCAGGTTCTTATATTGCTGCTACTATGGGTATCTGGCACCT
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APPLICANT: Park, John E.
APPLICANT: Bamberger, Uwe
APPLICANT: Bamberger, Uwe
APPLICANT: Bamberger, Uwe
APPLICANT: Bamberger, Uwe
APPLICANT: Saldanha, Jose W.
APPLICANT: Saldanha, Jose W.
APPLICANT: Saldanha, Jose W.
APPLICANT: Retrig, Wolfgang J.
ITLE OF INVENTION: RAP-specific Antibody with Improved Producibility
FILE REFERENCE: 0652.1890001
CURRENT APPLICATION NUMBER: US/09/301,593A
CURRENT FILING DATE: 1998-04-30
EARLIER APPLICATION NUMBER: EP 98107925.4
EARLIER APPLICATION NUMBER: US 60/086,049
EARLIER FILING DATE: 1998-05-18
NUMBER OF SEQ ID NOS: 108
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 27
LENGTH: 8068
           ACCCTATCATCCTCTGCAAGACAGTCCTCCCTCAAACCCACAAGCCTTCTGTCCTCACAG
                                                                                                                                       GAGCTTCAACAGGGGAGAGAGTGTTAGAGGGAGAAACTGCCCCCACCTGCTCCTCAGTTCCAG
                                                                                                                                                                                                                                                                                       AATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCTGTGGTTTCTCTTTTCC
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                                                                GAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAA
                                                                               GAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAA
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US-09-311-593-27
Sequence 27, Application US/09301593A
Patent No. 6455677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCCCCTGGGCCATGG 1499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-301-593-27
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APPLICANT: Park, John E.
APPLICANT: Banberger, Uwe
APPLICANT: Banberger, Uwe
APPLICANT: Leger, Olivier
APPLICANT: Leger, Olivier
APPLICANT: Saldamha, Jose W.
APPLICANT: Rettig, Wolfgang J.
TILE OF INVENTION: PRE-specific Antibody with Improved Producibility
FILE REFERENCE: 0652.1890001
CURRENT FILING DATE: 1990-04-29
EARLIER APPLICATION NUMBER: US (09/301,593A
CURRENT FILING DATE: 1998-04-30
EARLIER PILING DATE: 1998-04-30
EARLIER FILING DATE: 1998-04-18
SAFLIER FILING DATE: 1998-05-18
SOFTWARE: Patentin Ver. 2.0
SSETURENT FILING DATE: 1998-05-18
SOFTWARE: Patentin Ver. 2.0
GTGTTAGAGGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCTCCCATCC
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34.1%; Score 667.6; DB 4; Length 8068;
Best Local Similarity 75.1%; Pred. No. 5.2e-164;
Matches 973; Conservative 0; Mismatches 94; Indels 229;
                                                                                                                                  1264 ATAAATAAAGTGAATCTTTGCACCTGTGGTTTCTCT 1299
                                                                                                                                                ATAAATAAAGTGAATCTTTGCACCTGTGGTGGATCT 2663
                                                                                                                                                                                                                Sequence 35, Application US/09301593A Patent No. 6455677 GENERAL INFORMATION:
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US-09-301-593-35
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US-09-301-593-35
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July 18, 2003, 04:46:48; Search time 6294.87 Seconds · (without alignments) 10397.705 Million cell updates/sec
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2249
1 tctagaccaccatgggttgg......ccgggtaaatgagtgaattc 2249
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	228 Sequen	7 Homo	004 Sequen	339 Antibo	365	355 Sequence	379	AX088864 Sequence AX478054 Sequence	27 Seque	27	741 Seque	11.0	112	Human imm	AX327474 Sequence E06998 DNA encodin	Homo sapie	IO8115 Sequence 1 E10971 DNA sequenc	Sequence 5	DNA	Intron	Intr	Drug c Humani	Humanized		Humanized	Humanized	Humanized	ized		linear PAT 29-SEP-1999			., Rosa,M.D. and Rosa,J.J. rophylaxis and treatment of	
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* Query ore Match Length DB	2 79.7 2 2 79.7 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	.2 78.5 56310 .8 77.9 2193	6 73.4 2287	6 73.4 2287	.6 /3.4 2287 38 72.8 4694	38 72.8 4694	.8 71.7 4723	.8 71.7 4723 8 71.7 4723	8 71.6 2029	.8 71.6 2802 .6 71.5 169802	6 70.5 2482	6 70.5 2482	6 70.5 2482	.8 68.8 2252	8 2009	.2 68.8 2009	68.8 3133 68.7 2009	.6 68.7 2009	67.4 1980	.8 65.2 3108	.8 65.2 3147	.4 65.1 2071	.4 65.1 2071	.6 64.9 2077	6 64.9 2077	.4 64.7 2073	.4 64.7 2073	6 2073		AR035228 Sequence 44 from paten AR03-228	AR035228.1 GI:59518 Unknown.	Unknown. Unclassified. 1 (hases 1 to 2560)	Burkly, L.C., Chisholm, P. Anti-CD4 antibody homole	10 HIV 587173
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		1505 GGCCCGGCCGGCCCCCCCTCCTCCTCCTCCTCCGCGCCCTGGCTCCTGG 1564 1507 CAGCACCGGCGGCCCTGACGCCTCGGCCCTGGCGCCCTGGGCCCCGGGG 1564 1507 CAGCACCGTCGGTCTCCCCCCAAAACCCCAAGGACACCTCTCTGTGATCTCCCGGA 1524 1565 GGGGACCATCATCTCCCGGA 1624 1565 GGGGACCATCATCTCCCGGA 1624 1625 CCCCTGAGGTCACGTGGTGGTGGTGGTGGACGTCGACGCCCCAAGGACCCCCGAGGTCCCGGA 1626 1627 ACTGGTACGTGGTGGTGGTGGTGGACGTGAGCCACCAAGACCCCGAGGTCCAGTTCA 1684 1687 ACTGGTACGTGGGTGGAGGTGCATCATAATGCCAAGACCCCGAGGTCCAGTTCA 1686 1687 ACTGGTACGTGGGTGGAGGTGCATCATAATGCCAAGACCACGAGGACCAGTTCA 1686 1687 ACTGGTACGTGGGTGGAGGTGCATAATGCCAAGACCACGAGGACAGGTCCAGTTCA 1686 1687 ACTGGTACGTGGGTGGAGGTGCATAATGCCAAGACCAAGACCAGGAGGAGGAGGAGTTCA 1686 1687 ACTGGTACGTGGGTGGATGGATGATAATGCCAAGACCAAGACCAGGAGGAGGAGGAGGTGAAGGTTCAACAGGTCCTCCAAGACCAAGACCAGGAGGAGGAGGAGGAGGAGGAGGAG
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Source 1. 2560 Source 1. 2560 Organism="unknown" 448 t SE COUNT 544 a 848 c 720 g 448 t GOINT 544 a 848 c 720 g 448 t GOINT 544 a 848 c 720 g 448 t GOINT 80.2%; Score 1804; DB 6; Length 2560; Matches 2049; Conservative 0; Mismatches 185; Indels 64; Gaps RACCATGGGTTGGAACTGTATCATCTTTCTTTTGGTTACCACGTGTGCACTC	68 CCAGGTCCAACTGGTGCACTTGGGGGTGAAGAAGAGGTGGAAGATGTGGAAGATGGTGAAGATGGGGGTCCAACTGGTGGAGTTGAGGTGAAGAAGAGGTGTGAAGAGATGTGAAGAA	

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/db_xref="REMTREMBL:CAC12842"
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llarity 99.6%; Pred. No. 0;
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                join(<216. .509,902. .
/gene="IgG2"
/citation=[2]
/citation=[1]
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702 c 566 g
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902. .937
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Submitted (07-OCT-1999) Hougs L., Dept. of Clinical Immunology,
sect. 7631, National University Hospital, Rigshospitalet, Tagensvej
20, DK-2200 Copenhagen N., DENMARK
Related sequences 249801 and Z49802.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hougs, L., Svejgaard, A. and Barington, T.
The first constant-domain (CH1) exon of human IGHG2 is polymorphic and in strong linkage disequilibrium with the CH2 exon polymorphism encoding the G2m(n+) allotype in Caucasians
Immunogenetics 52 (3-4), 242-248 (2001)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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constant region; IgG2 gene; immunoglobulin; immunoglobulin heavy
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                                                                       AATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGACTCCGACGGCTCC
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Linkage and sequence homology of two human immunoglobulin pheavy chain constant region genes
Proc. Natl. Acad. Sci. U.S.A. 79 (6), 1984-1988 (1982)
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cell_type="lymphocytes"
tissue_type="blood"
/country="Denmark"
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'organism="Homo sapiens"
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chromosome="14"
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'clone="pigG2n+1"
'haplotype="G2m(n+)"
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Oy 1939 GTGTACACCCTGCCCCATCCGGGGGGGAGTGACCAAGA Db 1501 GTGTACACCTGCCCCCATCCGGGGGGAGTGACCAAGA Oy 1999 CTGGTCAAAGGCTTCTACCCCGGGGGAGTGACTGGCGTGGAGT Db 1561 CTGGTCAAAGGCTTCTACCCCAGCGACTCGCCGTGGAGT Oy 2059 GAGAACAACTACAAGACCACCTCCCATGGTGGAGTGC Oy 2119 AGCAACTCACCGTGGACCACCTCCCATGGTGGACTCCC Oy 2119 AGCAAGCTCACCTGGACAACAGACGACTGCCGGGGGGCGCACTCCCATGTTGGTGGACTCCCATGTTGATGTTCCCATGTTGATGATGTTCCCATGTTGATGATGTTCCCATGTTGATGTTCCCATGTTGATGTTCCCATGTTGATGTTCCCATGTTGATGTTCCCATGTTGATGTTCCATGTTCCATGTTCCATGTTCCATGTTCCATGTTCCATGTTCCATGTTCCATGTTCCATGTTCCATGTTCCATGTTCCATGTTCCATGTTCCATGTTCCATGTT	HUMIGCDI HUMIGCDI HUMIGCDI HUMIGCDI HUMAIGCDI HUMAIGCDI HUMAIGCDI HUMAIGCDI HUMAIGCDI HUMAIGCDI HUMAIGCDI HUMAIGCDI Jobaso SEGMENT SOURCE NOGANISM Homo saptiens ORGANISM Homo saptiens	genes were determined by Flanagan and Rab
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GTGGGAGAGCAATGGGCAGCCG 2058 On Mar 2, 2000 this sequence version replaced gi:32759.

[2] also reports sequences for gamma-3, gamma-4, and a gamma-pseudogene. Most of this sequence is 95* homologous with gamma-4. The hinge exons are only 70* homologous. The authors estimate that gamma-2 and gamma-4 and service of 6 million years ago. The authors in important role in tron-mediated domain transfer played an important role in the evolution of human gamma genes. They also report the hinge regions of gamma-1, gamma-4, and a pseudo-gamma gene. [1] estimates the divergence of the human gamma genes to be between 7.7 and 4.4 million years ago. This entry is part of a multigene region containing the gamma-2, gamma-4, epsilon-1, and alpha-2 genes. The relative locations of the four genes were determined by Flanagan and Rabbitts (Nature 300, 709-713 CCGACGGCTCCTTCTTCCTCTAC 2118 GGAACGTCTTCTCATGCTCCGTG 2178 GCCTCTCCCTGTCCCCGGGTAAA 2238 linear PRI 11-APR-2001 3: gamma-2 constant region, 11 to 1524) 0,T., Nakai,S. and Honjo,T. genes: implications for in human immunoglobulin of the gamma 2 and gamma 4 Vertebrata; Euteleostomi; ; Hominidae; Homo. an immunoglobulin gamma 84-1988 (1982)

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Matches 1801; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cranslation="STKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGA
(1982)). They refer to this gene group as region B. The region A genes are gamma-1, pseudo-epsilon, alpha-1. Flanagan and Rabbits also determined the general locations of the two regions. They place region A between the UH/mu/delta region and region B. Complete source information:
Human fetal liver DNA, library of T. Maniatis [3] and Lawn et al [2], [1]; clones p-gamma-2RPA3 [2], 5A [3], and Ig-gamma-2-15 [1].
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116. .508
| gene="limmunoglobulin heavy chain constant region CH1"
| 10. 901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | .901 | 
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                                                                                                                                                                                                                                                                                                                                                                                                      1. .215

| Gene="IgH"

| Join (<216. .509,902. .937,1056. .1382,1480. .1802)

| Gene="IgH"

| Godon start=3

| Product="immunoglobulin gamma-2 heavy chain"

| Protein id="AAB59393.1"

| Abaxef="GI:184758"
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                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/map="14q32.33"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16. .509
gene≃"IgH"
note="G00-119-338"
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38. .1055
gene="IgH"
                                                                                                                                                                                                                                                                                                                                    <li. .2009
/gene="IgH"
/note="IGHG2"
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gene="IgH"
citation=[3]
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gene="IgH"
citation=[3]
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gene="IgH"
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/gene="IgH"
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8 6 7 8 8 9 8 8 9 8 8 9 8 9 8 9 8 9 9 8 9	Research, 320 Charles Street, Cambridge, MA 02141, USA On Jan 15, 2001 this sequence version replaced gi:11120856 All repeats were identified using RepeatMasker:
Db Db 1 Oy 1 Oy 1 Oy 2 Db 1 Oy 2 TITLE AUTHORS TITLE AUTHORS	COMMENT
130	1819 AAGGTGGGACCCGCGGGGTATGAGGGCCACATGGACAGAGGCCGGCTCGGCCCACCTCT

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23946
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                                                                                                                                                                                           23947 TCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                        Center cloud name: 815_P.21
Sequencing vector: Plasmid; n/3; 100% of reads
Sequencing vector: Plasmid; n/3; 100% of reads
Chemietry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 55130 bases at least Q40
Consensus quality: 55683 bases at least Q30
Consensus quality: 56050 bases at least Q20
Insert size: 61000; agarose-fp
Insert size: 56110; swm-of-contigs
Quality coverage: 7.9 in Q20 bases; sum-of-contigs
Quality coverage: 8.6 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 56310;
                               http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                  Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
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clone="RP11-815P21"
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Best Local Similarity 98.9%;
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LEWIGG1YPCORNDFFKTORAKLTAVTSANTAYMELSSLTNEDSAVYYCSIIYPD

YADFIMDYWGGTTYTVORYFRSTKGPSVFPLAPCSSSTSESTRALGGLVKDYFPEPPTV

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VERKCCVECPPCPAPAPAGPSVFFPFPRYNCTLMISRTPEVTCVVUVSKHEDPEVQFY

WYDGYPUNTAKTREREGFSNSTFRYVSVLTVVNSTAVTVNSKGLAPADIEK

TISKTKGOPREPQYTLPPSREEDFTCLVKGFYPSDIAVENSKGLAPADIEK

TISKTKGOPREPQYTLPPSREEDFTCLVKGFYPSDIAVENSNGOPENNYK

TTPPPILDSDGSFFLYSKLTVDKSRWQQGNVFSCSVWHEALHNHYTQKSLSLSPGK"
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7; Mismatches 109;
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Eutheria; Primates; Catarrhin; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

I (bases 1 to 2193)

Activity of human igg and igg subclasses in immune defense against neinseria meningitidis serogroup B

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E 2 (bases 1 to 2193)

S Vidarsson, G., Jansen, M., Boel, E. and van de Winkel, J.G.J.

Ly inmunol. 166 (10), 6250-6256 (2001)

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S Vidarsson, G., Jansen, M., Boel, E. and van de Winkel, J.G.J.

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AF237584 GI:9857754
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GGAACTCAGGCGCTCTGACCAGCGGGGGGCACCATCCCAGCTGTCCTACAGTCCTCAG	TGCTTGGCTCAGACCTGCCAAAAGCCATATCCGGGAGGACCCTGCCCCTGACCTAAGCCG 12 [1495 CACCACCTGGGGCACCCTCAGTCTTCCTCTTCCCCCAAAACCCAAGGACACCCTCA 1554 1337 CACCACCTGGGGCACCCTCAGTCTTCCTTTCCCCCCAAAACCCCAAGGACCCTCA 1396 1555 TGATCTCCCGGACCCCTGAGGTCATCCTTTCCTTTCCCCCAAACCCCAAGACCCTCA 1396 1555 TGATCTCCCGGACCCCTGAGGTCACGTGGTGGTGGACGTGAGCCACCAAGACCCC 1614 1397 TGATCTCCCGGACCCCTGAGGTCACGTGGTGGTGGTGGACGTGAGCCACGAAGACCCC 1456 1615 AGGTCCAGTTCAACTGGTACGTGGACGGCGTGGACGTGAGCCAAGACCCC 1674 1457 AGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTCAATGCCAAGACCAC 1516 1675 GGGAGGAGCAGTTCAACAGGACGTCCGTGGTGGTCATAATGCCAAGACCAC 1516 1675 GGGAGGAGCAGTTCAACAGGACGTCCGTGGTCACACAAGACCACCAGG 1734 1517 AGGTCCAGTTCAACTGGTACAAGTGCAAGGTCCCCCACCCCCCCC

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CCCAAAGGCCAAACTGTCCACTCCTCAGCTCG 1289 1400 1430 CCCCGGCTGTGCAGCCCCAGGCCAGCAA 1049 AAGCCTCTGCCCGCCCCACTCATGCTCAGGGA 1109 CTTGGCTCAGACCTGCCAAAAGCCATATCCGGG 1229 BAGTAGCCTGCATCCAGGGACAGGCCCCAGCTG 1460 rccrcagcacc---accrececaecaccerca 1517 SCCACGAAGACCCCGAGGTCCAGTTCAACTGGT 1632 CGTTGTGCACCAGGACTGGCTGAACGGCAAGG 1752 SCCTCCCAGCCCCCATCGAGAAAACCATCTCCA 1812 CCAGCTCAGGGAGGAGGGTGTCTGCTGGAAGC 989 CTCTGGGCAGGCACAGGCTAGGTGCCCCTAACC 1190 GTTCCTGTGGGAGTACTAGAGGGCCTGGGGAC 1605 SAGGCCACATGGACAGAGCCGGCTCGGCCCA 1905 CCAACCTCTGTCCCTACAGGGCAGCCCCGAGAA 1932 TCCAGGCAGGCACAGGCTGGGTGCCCTACCC 1169 BACACCCTCATGATCTCCCGGACCCCTGAGGTC 1577 PAGGGCCACATGGACAGAGGCCGGCTCGGCCCA 1872 CTCTACTCCCTCAGCAGCGTGGTGACCGTGCCC 894 ACCTGCAACGTAGATCACAAGCCCAGCAACACC 929 COTGCCCAGGTAAGCCAGCCCAGGCCTCGCCCT

63 CACTCCCAGGTCCAGCTGGTGCAGTTGGGGCTGAGGTGAAGAAGCCTTGGGAGCTCAGTG 122	CAGGCCCCTGGACAAGGCTTGAGTGGATGGAGGATCATCCTATCTTTGGTACAGCA AACTACAACCAAGGCTTTAAGGGCAAGGCAA	303 GCCTATATGGAACTTAGTGATCTTGAGGATACGGCCGTTTATTACTGTGCAAGA 362	390 CAAGGTACCCTTGTCACCGTCTCCTCAGGTGAGTCCTTAAAACCTCTAGAGCTTTCTGGG 449	CCAGCCAGTGCACCCCAATGCCCGTGGACCCCAGACTGGACCCTGCTCGCCTCGCTCG		690 CCCTGCTCCAGGGACCTCCGAGAGCACAGGGCCCTGGGCTGGTCAAGGACTAC 749	810 TTCCCAGCTGTCCTACAGTCCTCCAGGACTCTCACCCTCAGCAGCGTGGTGACCGTGCCCCCCCC	895 TCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGGCCCAGCAACAC 954 930 AAGGTGGACAAAAGTTGGTGAGAGGCCAGCTCAGGAGGGAG	990 CAGGCTCAGCCTCTGCAGACGCACCCCGGCTGTGCAGCCCCAGGGCAGCAA 1049
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	PRESULT 9 190051	Ouery Match 73.4%; Score 1651.6; DB 6; Length 2287; Best Local Similarity 87.2%; Pred. No. 3e-311; Matches 1998; Conservative 0; Mismatches 219; Indels 75; Gaps 14;	Oy 6 ACCACCATGGGTTGGAACTGTATCATCTTTCTGGTTACCACAGCTGTG 62	Oy 63 CACTCCCAGGTCCAGCTGCAGTCTGGGGCTGAGGTGAAGAACCTGGGAGCTCAGTG 122	Oy 123 AAGGTGCCTGCAAAGGTTCCGGCTACACATTCACTGATTATGCTATACGTGGGTGAGA 182	Oy 183 CAGGCTCCTGGACAGGGCCTCGAGTTGGAGTTATTAATATTATAGATAATACA 242	Oy 243 AACTACAACAGAAGTTTAAAGGGCAAAGGCCACAATGACTGTAGACAAGTCGACGAGCACA 302	Oy 303 GCCTATATGGAACTTAGTTCTTTGAGGATACGGCCGTTTATTACTGTGCAAGA 362	Oy 363 GCGG	Oy 390 CAAGGTACCTTGTCACCGTCTCCTCAGGTGACTCTTAAAACTCTTAGGG 449	Qy 450 GCGAGCCGGGCCTGACTTTGGCTTTGGGCCAGGGGGCTAAGGTGAGGCAGGTGGCG 509	Qy \$10 CCAGCCAGGTGCACACCCCAATGCCCGTGAGCCCAGACACTGGCCTGGCTCGACCCTCG \$69 b	
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CTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC 2172
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1 (bases 1 to 4694)
Korman,A.J., Halk,E.L. and Lonberg,N.
Human ctla-4 antibodies and their uses
Patent: WO 0114424-A 41 01-MAR-2001;
MEDAREX, INC. (US)
Location/Qualifiers
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Similarity 94.6%; Pred. No. 1.2e-308; Conservative 0; Mismatches 95; Indels 4; Gaps AACTGTAGAGGTTTGGGGGGAGGCGGGCTGACTTTGGCTTTGGGAAGGAGGGGGGAAGAGGGAGG	67 CTAAGGTGACGCAGGCGAGGTGCACAATGCCCAATGCCCATGACCCAAACCT 126 550 GGACCCTGCCTGGACCCTGGGATAGACAAGAACCGAGGGGCCTCTGCGCCCTGGGCCC 619	610 AGCTCTGTCCCACACGGGGTCACATGGCACCACCTCTTGCAGCCTCCACCAAGGGCC 669 187 AGCTCTGTCCCACACGGGGTCACATGGCACCACTCTCTTGCAGCTTCCACCAAGGGCC 246	carcgercrrccccrgccccrgcrccagagcaccrccagagcacacagcgcccrg 7	GCTGCCTGGTCAAGGACTACTTCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCTC 78 [790 TGACCAGCGGCGCACCTTCCCAGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCA 849	850 GCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCTACACCTACACGTAG 909 	910 ATCACAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGGTGAGAGGCCACCTCAGGGAG 969 	970 GGAGGGTGTCTGCTGGAAGCCAGGCTCCAGCCCTGCTGGACGCACCCCGGCTGTGCA 1029	1030 GCCCCAGCCCAGGAGGCAGGCCCCATCTGTCTCCTCACCCGAAGGCCTCTGCCC 1089	1090 GCCCCACTCATGCTCAGGAGAGGTCTTCTGGCTTTTTCCACCAGGCTCCAGGCAGCA 1149 	1150 CAGGCTGGGTGCCCCTACCCCAGGCCCTTCACACAGGGGCAGGTGCTTGGCTCAGACC 1209 	1210 TGCCAAAAGCCATATCCGGGAGGACCCTGCCCCTGACCTAAGCCGACCCAAAGGCCAAA 1269 	1270 CTGTCCACTCCGTCAGCTCGGACACCTTCTCCTCCCAGATCCGAGTAACTCCCAATCT 1329 	1330 TCTCTCTGCAGAGGGCAAATGTTGTGTGAGTGCCCACCGTGCCCAGGTAAGCCAGCC	1390 GGCCTCGCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCATCCAGGGACA 1449	1450 GGCCCCAGCTGGGTGCTGACACGTCCATCTTTCTCAGCACCACCTGCGG 1506

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B), which includes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [1] reports that the human C-gamma-4 gene is equally homologous to the mouse gamma-1, gamma-2a, and gamma-2b genes (about 75%). [3] also reports partial sequences for human gamma-2, gamma-3, and a gamma pseudogene. [2] presents the gamma-1, gamma-2, gamma-3, and fins entry is part of a multigene region (region B), which includes the gamma-2, gamma-4, epsilon-1, and alpha-2 genes. See segment 1
                                                                                                                                                                                                                                                                                                                                                                                                        (bases 475 to 1069; 1180 to 1331; 1432 to 1655)
Takahashi,N., Ueda,S., Obata,M., Nikaido,T., Nakai,S. and Honjo,T.
Structure of human immunoglobulin gamma genes: implications for evolution of a gene family
Cell 29 (2), 671-679 (1982)
                                                                               in human immunoglobulin
of the gamma 2 and gamma
                                                                                                                                                                                                                                                                                           gamma
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Human fetal liver DNA, library of T. Maniatis [3] and Lawn et a [1], [2]; clones 24B [1], lambda-HG4.1 [3], and Ig-gamma-4-2 [2] Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <1. .215
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/note="gamma-4 intron J-C"
join(<216. .509,900. .935,1054. .1383,1481. .1803)
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                                                                                                                                                                                                                                                                              Linkage and sequence homology of two human immunoglobulin heavy chain constant region genes Proc. Natl. Acad. Sci. U.S.A. 79 (6), 1984-1988 (1982)
                          2 (bases 894 to 1106)
Comparison of the hinge-coding segments gamma heavy chain genes and the linkage (BMBO J. 1 (4), 403-407 (1982)
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Ellison, J. and Hood, L.
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FEATURES Location/Qualifiers SOURCE 1. 4723 Arganism="unknown" BASE COUNT 1072 a 1411 c 1253 g 987 t ORIGIN	Query Match 71.7%; Score 1611.8; DB 6; Length 4723; Best Local Similarity 94.3%; Pred. No. 1.5e-303; Matches 1722; Conservative 0; Mismatches 87; Indels 18; Gaps	Qy 430 AACCTCTAGAGCTTCTGGGGCGGGGCCTGACTTTGGCTTTGGGGAGGGGTGGG 489	Qy 490 CTANGGEGGGGGGGGCGGGGGGGGGGACACCCAATGCCCGGGGGCCCAGACACT 549 Db 68 CTANGGTGAGGCAGGTGCCAGCCAGGTGCACACCCAATGCCCATGAGCCCAGACACT 127	QY 550 GGACCCTGCCTGGACCCTCGTGGATAGACAAGAACCGAGGGCCTCTGCGCCCTGGGCCC 609 Db 128 GGACCTGAACCTCGCGGACAGTTAAGAACCCAGGGCCTCTGCGCCCTGGGCC 182	Qy 610 AGCTCTGTCCCACCACCGCGGTCACACGCCTCTCTTGCAGCCTCCACCACGCGC 669 Db 183 AGCTCTGTCCCACACGCGGTCACGACGCCCACCACCTCTTGCAGCCTCCACCAGGGCC 242	Qy 670 CATCGGTCTTCCCCTGGCGCCCTGGTCCAGGAGCACTCCGAGAGCACAGGGCCCTGG 729	Qy 730 GCTGCCTGGTCAAGAACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCCAGGCGCTC 789	Qy 790 TGACCAGGGGGTGCACCTTCCCAGGTGTCCTACAGTCCTCAGGACTCTACAGTCCCTCA 84.	Qy 850 GCAGCGTGGTGACCGTCCCCCCCCCCCACACCTACACCTACACCTACACCTACACCTACACCTACACCTACACCTACACGTACACCTACACACCTACACCTACACCTACACCTACACCTACACCTACACCTACACCTACACCTACACCTACACCTACACCTACACCTACACCTACACCTACACCTACACACCTACACACCTACACACCTACACACCTACACACCTACACACCTACACACACCTAC	QY 910 ATCACAAGCCAGCAACACCAAGGTGGACAAGACAGTGGAGAGGCCAGCTCAGGGAG 969 LIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	QY 970 GGAGGGTGTCTGCTGGAAGCCAGGCTCAGCCTCCTGCTTGGACGCACCCCGGCTGTGCA 102 Db 543 GGAGGGTGTCTGCTGGAAGCCTGGGCTCAGCGCTCTGGACGCATCCCGGCTATGCA 602	Qy 1030 GCCCGAGCCCAGGGCAGCAGCCCCATCTGTCTCTCACCCGAGGCCTCTGCCC 1088	Qy 1090 GCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCCACCAGGCTCCAGGCAGG	OY 1150 CAGGCTGGGTGCCCTACCCCAGGCCTTCACACACAGGGGCAGGTGCTTGGCTCAGACC 120:	OY 1210 TGCCAAAAGCCATATCCGGAAGACCCTGCCCCTGACCTAAGCCGACCCCAAAGGCCAAA 126:	OY 1270 CTGTCCACTCCCTCAGCTCGGACACCTTCTCTCCTCCCAGATCCGAGTAACTCCCAATCT 1328	Qy 1330 TCTCTGCAGAGCGCAAATGTTGTGCGAGTGCCCACCGTGCCCAGGTAA 1380
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٥٧	1381 GCCAGCCCAGGCCTCGCCTCCAGGCGGGACAGGTGCCCTAGAGTAGCCTGCAT 1440	TITLE Human ctla
qq	962 GCCAGCCCAGGCCTCGCCTCCAGCTCAAGGCGGGACAGGTGCCTAGAGTAGCCTGCAT 1021	_
٥٨	1441 CCAGGGACAGGCCCCAGCTGGGTGACAGCTCCACCTCCATCTTTCCTCAGGACC 1498	FEATURES I
QQ	1022 CCAGGGACAGCCCCAGCCGGGTGCTGACACGTCCATCTCTTCCTCAGCACCTG 1081	
ò	1499 -ACCTGCGGCAGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGA 1557	BASE COUNT 1072 a
ΩÞ	1082 AACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAACCAAGGACACCTCATGA 1141	ORIGIN
ò	1558 TCTCCCGGACCCCTGAGGTCACGTGGTGGTGGACGTGAGCCACGAAGACCCCGAGG 1617	Query Match Best Local Similarit
QQ	1142 TCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGTGAGCCCACGAAGACCCTGAGG 1201	Matches 1722; Conse
è		Qy 430 AACCTCTA
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l è		Qy 490 CTAAGGTG
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à ·	1738 GGCTGAACGCCAAGGAGTACAAGTGCAAGGTCTCCCAAGGCCTCCCAGCCCCCATCG 1797	Db 128 GGACGCT-
Q	1322 GGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAAAAAAGCCCTCCCAGCCCCATCG 1381	
ò	1798 AGABAACCATCTCCAAAACCAAAAGGTGGGACCCGCGGGGTATGAGGGCCACATGGACAGA 1857	
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qq	1442 GGCCGGCTCGGCCCACCCTCTGCCCTGAGAGTGACCGCTGTACCAACCTCTGTCCCTACA 1501	Db 243 CATCGGTC
ò	1918 GGGCAGCCCCGAGAACCACAGGTGTACACCCCTGCCCCATCCGGGAGGAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAG	Qy 730 GCTGCCTG
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ctla-4 antibodies and their uses
: WO 0114424-A 40 01-MAR-2001;
X, INC. (US)
Location/Qualifiers
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/bx zref="taxon:32630"
/note="gammal heavy chain plasmid pC
2 a 1411 c 1253 g 987 t 1150 1210 722 782 a y ò g ò

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AXO88864 4723 bp Sequence 40 from Patent WO0114424. AXO88864 AXO88864.1 GI:13397635

RESULT 14
AX088864
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DEFINITION
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KEYWORDS
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synthetic construct. synthetic construct artificial sequences. 1 (bases 1 to 4723)

REFERENCE

VERSION AX478054.1 GI:22217036 KEYWORDS SOURCE SYNTHetic construct. ORGANISM synthetic construct. ORGANISM artificial sequences. REFERENCE Transperson cranschronosomal rodents for making human antibodies TTTLE TTTLE TRANSPERSON CO 243478-A 2 06-UND-2002; DOURNAL Patent: WO 0243478-A 2 06-UND-2002; DOURNAL Patent: WO 0243478-A 2 06-UND-2002; FEATURES LOCATION (US) ; KIRIN BEER KABUSHIKI KAISHA (JP) FOURCE // 1723	Ouery Match Duery Match Best Local Similarity 94.3%; Pred. No. 1.5e-303; Batches 1722; Conservative 0; Mismatches 87; Indels 18; Gaps 4; Oy 430 AACTCTAGAGGGGGGGGGGGGCTGGGCTTTGGGCTTTGGGGCAGGAGGGGG 489 Db 8 AGCAGTGAAGCTTCTGGGGCAGGCCAGGCCTGACCTTTGGGCAGGAGGGG 67 Oy 490 CTAAGGTGAGGTGAGGTGGCGCAGGCCAGAGGCCGGGGGGGG			850 GCAGGTGGTGACCTCCAGCAGCTGTCCTACAGTCCTCAGGACTGTACTCTCAGGACTGCAACGTAG 850 GCAGGTGGTGACCTCCAGCAACTTCGGCACCCAGACCTACACTCTGCAACGTAG 11	543 GGGGGGGGGGGGGGCGCGTCTGGGGGCTCCTGGCTGGGGCTTGGGGCTTGGGGCTTGGGGCTTGGGGCTTGGGGCTTGGGGCTGGTGG	Qy 1150 CAGGCTGGGTGCCCTACCCCAGGCCCTTCACACAGGGGCAGGTGCTTGGCTCAGACC 1209
	1082 AACTCCTGGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCCAAGGACACCCTCATGA 114 1558 TCTCCCGGACCCCTGAGGTCACGTGCTGGTGGACGTGAACCCCAAGAACCCCCAGG 161 1142 TCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAACCCAGAAACCCCTGAGG 120 1618 TCCAGTTCAACTGGTACGTGAGGTGGTGGTGGTGACGTGAACCCAAAACCCAGGG 167 1202 TCAAGTTCAACTGGTACGTGAGGGGGGGGGGGGTGCATAATGCCAAAAACCCAGGG 167 1202 TCAAGTTCAACTGGTACGTGAGGGGGGGGGGGGGGTGCATAATGCCAAAAACCCAGGG 167 1202 TCAAGTTCAACTGGTACGGGGGGGGGGGGGGGGGAGAAAACCCAGGG 126	1678 AGGACCAGTTCAACAGCACGTTCCGTGGCTCACCGTTGTCGCACCAGGACT 1 1262 AGGACCAGTTCAACAGCACGTACCGTGTGGTCACCGTTGTCACCGTTGTCACCGTTGTTGTCACGTTGTTGTCACGTCTCACCGTCCTGCACCGGACT 1 1262 AGGACCAGTAACAGCACGTACCAGTGTCAACAGCGTCCTCCACCGTCCTGCACCGGACT 1 1322 GGCTGAACGGCAAGAGTACAAGTGCAAGGTCTCCAACAACAAGGCCTCCCAGCCCCCATCG 1 1322 GGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAAGCCCCCCATCG 1 136 AGAAAACCATCCCAAAACCAAAGGTGCAAGGGCCCCCCATCG 1 1798 AGAAAACCATCTCCAAAACCAAAAGGTGGGACCCCCCCATCG 1 1791	1812 AGAMARICATICTICARANGCICAGIGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	Db 1562 ACCAGGTCAGCTGACCTGGTCAGAGGTTCTATCCCAGGGACATCGCGTGGGG 1621 1621 1621 1621 1621 1621 1621 1621 1622 1621 1622 162		LOCUS AX478054 4723 bp DNA linear PAT 12-AUG-2002 DEFINITION Sequence 2 from Patent W00243478.

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Search completed: July 18, 2003, 13:47:32 Job time: 6302.87 secs

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BI768933 856 bp mRNA linear EST 25-SEP-2001
603058055F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5207605 5',
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603617582
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can befound through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov m. a. column: 14
High quality sequence stop: 797.
Location/Qualifiers
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(bases 1 to 856)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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BG398446 602439729
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BG75349 602713669
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                                                                   July 18, 2003, 04:16:54; Search time 3897.3 Seconds (without alignments) 9345.860 Million cell updates/sec
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Maximum Match 100%
Listing first 45 summaries
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Score

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Post-processing: Minimum DB seq Maximum DB seq

Database

Scoring table:

Perfect score:

Sequence:

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Run on:

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/note="Cells", Vector: potB7, Vector: potB7, Site=1: XhoI;
/note="Cells", Vector: potB7, 
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota, Metazoa; Chordata; Catarrhini; Hominidae; Homo.

In (bases 1 to 974)

Standard Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: Gapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Plate: LLCM1281 row: j column: 07

High quality sequence stop: 801.

High quality sequence stop: 801.
                                                                                                                 BG198446 974 bp mRNA linear EST 12-MAR-2001 (2013)9799F1 NIH MGC_48 Homo sapiens cDNA clone IMAGE:4565862 S', mRNA sequence. BG198446 BG198446.1 GI:13291894
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/organism="Homo sapiens"
/doratism="Homo sapiens"
/doratism=traxon:9606"
/clone=lib="NIHAGE:527605"
/clone=lib="NIH MGC_122"
/lab host="DH10B"
/lab host="DH10B"
/note="Organ: pool of 24 week female lung, 16 week female sanoimous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dryimed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note: this is a NIH MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1486 CTTCCTCAGCACCACCAGCAGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGG 1545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1906 TCTGTCCCTACAGGGCAGCCCCGAGAACCACGGTGTACACCCTGCCCCATCCCGGGAG 1965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1966 GAGATGACCAAGAACCAGGTCAGCCTGACCTGGTCAAAGGCTTCTACCCCAGCGAC 2025
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          426 -----AGGGCAGCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAG 474
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23.7%; Score 533; DB 13; Length 856;
Best Local Similarity 85.8%; Pred. No. 2e-118;
Matches 646; Conservative 0; Mismatches 10; Indels 97; Gaps
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AGGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCC 1791
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCATCGAGAAAACCATCTCCAAAACCAAAGGTGGGACCCGGGGGTATGAGGGCCACATG 1851
/clone_lib="NCI_CGAP_Skn3"
/lab_host="DP108 (Ti_phage-resistant)" | Site_1: NotI;
/lab_host="DP108 (Ti_phage-resistant)" | Site_1: NotI;
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT Average insert size 1.5kb. Library constructed by Life
Average insert size 1.5kb. Library constructed by Life
Tothologies. Note: this is a NCI_CGAP_Library."
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                                                                                                                                                                                             97;
                                                                                                                                                        22.5%; Score 506.4; DB 12; Length 757; ilarity 83.5%; Pred. No. 5.5e-112; Conservative 0; Mismatches 27; Indels 97;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 757)

S NIH-MGC http://mgc.nci.nih.gov/.

Mational Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1959)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: James Cleaver, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Thc.

CLORA Library Arrayed by: Thc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Http://mage.llnl.gov

Plate: LLAM10594 row: b column: 07
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602620925F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4746150
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                                 AAGCCGCGGGAGGAGCAGTACACACGTACCGTACCGTCAGCGTCCTCACCTCACCTC
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                                                                                                       362 CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAAGCCCTCCCA
                                                                                                                                           GCCCCCATCGAGAAACCATCTCCAAAACCAAAGGTGGGACCCGCGGGGGTATGAGGGCCA
                                                                                                                                                                                                            .848 CATGGACAGAGGCCGGCTCGGCCCACCTTGGCCTGGGAGTGACCGCTGTGCCAACCTC
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TGGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGA-GCTCTGCACAAC--AT
                                                                                                                                                                           GCCCCCATCGAGAAACCATCTCCAAAGCCAA----
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Location/Qualifiers
1. .757
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BG674795.1 GI:13906191
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1 (Dases; 1 to 871)

2 NIH-McG http://mgc.ndi.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Libra at:
http://image.lln.gov
Plate: LicMcSes row: k column: 02
High quality sequence stops: 848.

Location/Qualifiers
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602709506F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4846201 5',
mRNA sequence.
BG753979
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Pred. No. 2e-111;
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658 AAGAGCCTCTCCCTGTCTCCGGGTAAATGAGTG 690
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                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Entaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

I (Dases 1 to 990)

NIH-MGC http://mgc nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Contact: Preparation in M.G.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Hoth; //image Illn.gov

Plate: LLCM1700 row: j column: 18

High quality sequence stop: 782.

Location/Qualifiers
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BG754808 GI:14065461
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                                              CCGAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGC
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                                                                                     TCATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACC
                                                                                                                                                           CTGAGGTCAAGTTCAACTGGTACGTGGACGCGTGGAGGTGCATAATGCCAAGACAAAGC
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
 Gaps
97;
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28;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="InvAge="84621"
/clone="InvAge="84621"
/clone="InvAge="84621"
/clone="InvAge="primary" B-cells from tonsils (cell line)"
/lab host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoR1; cDNA made by oligo-dT priming.
Directionally cloned into EcoR1/XhoI sites using the following 5' adaptor: GGACGAGG(0). size-selected >SObbp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library " 1 others
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Tissue Procurement: Louis M. Staudt, M.D., Ph.D. cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) and Sequencing by: Tincyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.lln.gov lablate: LLCMI702 row: i column: 22 high quality sequence stop: 779. High quality sequence stop: 779.
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I (Dases 1 to 983)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Ontanal Institutes of Health, Mammalian Gene Collection (MGC)

Londat: Robert Strausberg, Ph.D.

Email: cgapba: r@mail.nih.gov

Tissue Procurement. Dr. Mark Watson

CONA Library Preparation: Rubin Laboratory

Tissue Procurement. The I.M.A.G.E. Consortium

CDNA Library Arrayed by: The I.M.A.G.E. Consortium

CONA Library Arrayed by: The I.M.A.G.E. Consortium

CONA Library Arrayed by: The I.M.A.G.E. Consortium/LIML)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LIML at:

Clone distribution: MGC clone distribution information can be

http://magg.lln.gov

Plate: LLOM2469 row: k column: 12

High quality sequence stop: 604.

Location/Qualifiers

1. 983

Lordanism="Homo sapiens"

/db xref=""Hum Gene" place" prompty: site 1: XhoI; Site 2:

Clone="IMAGE: 6279683"

/clone="IMAGE: 6279683"

/clone="IMAGE: 6279683"

/clone="IMAGE: 6279683"

/clone="IMAGE: 6279683"

/clone="IMAGE: 6279683"

/clone="IMAGE: 6279683"

/clone="MAM made by oligo-dT priming. Directionally cloned into Rocal/CAAG(G). Library constructed by Ling Homy in the laboratory of Gerald M. Rubin (University of Carliconia, Suberscript LIRI (Life Technologies). Note: this is a NIH-MGC Library.
                                                                                                                                                                                                                                                                               BQ708975
983 bp mRNA linear EST 16-JUL-2002
AGENCOURT 8353514 NIH_MGC_113 Homo sapiens CDNA clone IMAGE:6279683
5', mRNA Sequence.
BQ708975.1 GI:21847874
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GACTCCGACGCCTCCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 2151
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                                                                                                             630
                                    511 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
                                                                                                 571 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG
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22.4%; Score 504.2; DB 14; Length 983;
Best Local Similarity 83.4%; Pred. No. 2.1e-111;
Matches 628; Conservative 0; Mismatches 28; Indels 97;
                                                                                                                                              AAGAGCCTCTCCCTGTCCCCGGGTAAATGAGTG 2244
                                                                                                                                                                          631 AAGAGCCTCTCCCTGTCTCCGGGTAAATGAGTG 663
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AGENCOURT 8418162 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6281403
5', mRNA sequence.
BQ712021
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295 AGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCC
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Query Match
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/clone="IMAGE:6281403"
/clone lib="NIH MGC 113"
/lab hogt="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/KhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
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RESULT 9 BQ708562

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1. 873

/ organism="Homo sapiens"
/ db_xref="Laxon:8606"
/ clone="IMAGE:6215950"
/ clone=lib="NIH_MGC 113"
/ lab_host="HHJDB (phage-resistant)"
/ lab_host="HHJDB (phage-resistant)"
/ loce="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2: EOSI; cDNA made by Oligo-dT priming. Directionally cloned into ECORI/XhoI sites using the following 5' adaptor: GGGAGGG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NTH MGC Library."
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          mRNA linear EST 16-JUL-2002 sapiens cDNA clone IMAGE:6215953
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
Email: ggapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Bioscience Corporation
DnA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2385 row: I column: 02
High quality sequence stop: 682.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Pred. No. 4.9e-111;
3; Mismatches 29;
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SGENCOURT 8353965 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6278583
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Bukaryota; Detheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 947)
NHT-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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AGENCOURT 8485151 NIH_MGC_113 Homo sapiens CDNA clone IMAGE:6301245
5', mRNA sequence.
BQ709152
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                                     1912 CCTACAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATG 1971
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                                                                    ----AGGCCAGCCCCGAGAACCACAGGTGTACACCCCTGCCCCCATCCCGGGATGAGCTG
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/lab host="NHH MGC_113"
/note="Vorgan: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
Cnote="Vorgan: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
ECRI; cDNA made by oligo-dT priming. Directionally cloned
into ECORI/XhoI sites using the following 5' adaptor:
GGCAGGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-CNNA synthesis kit (Stratagene) and
Supergript II RT (Life Technologies). Note: this is a
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.Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LiCM2466 row: m column: 16
High quality sequence start: 3
High quality sequence stop: 675.
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Pred. No. 5.1e-111;
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                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6278583"
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22.3%;
Best Local Similarity 83.3%;
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/organism="Homo sapiens"
/db xref="taxon:966"
/db xref="IMAGE:627599"
/clone=lib="IMAGE:627599"
/clone lib="NHH MGC 113"
/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: poTB7; Site_1: Xho1; Site_2: FoORI; CDNA made by oligo-dT priming. Directionally cloned into BcoRI/Xho1 sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis Kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a
                                                                                                                             2211
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AGENCOURT 8352308 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6277592
S', mRNA Sequence.
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S NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
L Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs.r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The 1.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2464 row: d column: 09
High quality sequence stop: 640.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                       1152 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACACACCACTACACGCAG

191 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACCACCACCACCACGCAG
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GACTCCGACGGCTCCTTCTTCCTCTACAGCACACCTCGTGGACAAGAGCAGGTGGCAG
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Pred. No. 9e-111;
0; Mismatches 30; Indels
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/clone="IMAGE:6214450"
/clone="Inb="NIH MGC 113"
/lab host="DHIH MGC 113"
/lab host="DHIH MGC 113"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2: EoRI; CoDM made by oligo-dr priming. Directionally cloned into EcoRI/KhoI sites using the following 5' adaptor: Into EcoRI/KhoI sites using the following 5' adaptor: EoRACAGGG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis Kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library and 1297 c 229 g 150 t 9 others
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                                                                                                                                                                                                                      cch 22.3%; Score 501; DB 14; al Similarity 83.1%; Pred. No. 1.2e-110; 626; Conservative 0; Mismatches 30;
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919 bp mRNA linear EST 16-JUL-2002
AGENCOURT 7976429 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6214450
5', mRNA Sequence.
BQ709339
BQ709339.1 GI:21848238
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NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Conteat: Robert Strausberg, Ph.D.

Email: egapbs-remail.nih.gov

Tissue Procurement: Dr. Mark Watson

CDNA Library Preparation: Rubin Laboratory

CONS Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: Lic/M2381 row: m column: 11

*High quality sequence stop: 576.
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Mammallai Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 919)
                                                                                 AGGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCC
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                                                                                                               <u>AGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAGAGCCCTCCCAGCCC</u>
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/db_xref="taxon:9606"
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514

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2164

574

634

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

E 1 (Bases I to 843)

I (Bases I to 843)

I Unpublished (1999)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Mark Watson

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CON Library Preparation: Ling Cone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Http://image.lll.gov

Plate: LLCM1939 row, d column: 22

High quality sequence stops: 833.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BM007897 843 bp mRNA linear EST 30-OCT-2001
60617582F1 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5450469 5',
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    335 CCCGAGAACCACAGGTGTACACCCTGCCCCATCCCGGGAGGAGATGACCAAGAACCAGG
                                                                      395 TCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGA
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0; Mismatches 29;
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22.2%;
Best Local Similarity 83.2%;
Matches 624; Conservative C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db xref="taxon:9606"
/clone="IMAGE:4776923"
/clone=lib="NCI CGAP_SKN3"
/lab host="UNIOR TI phage-resistant)"
/lab host="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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                                                                                                                                                                                    Euteleostomi;
                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Clone Library Arrayed a column: 12
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                                                                                                                                                      Homo sapiens Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostoi Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 797) NIH-MGC http://mgc.nci.nih.gov/. NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGCAGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCG
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Pred. No. 1.8e-110;
0; Mismatches 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         quality sequence stop: 782.
Location/Qualifiers
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                                                                                         BG741164.1 GI:14051817
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Similarity 84.3%;
18; Conservative
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COMMENT
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q	139 CACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACCCC	
δλ	1552 TCATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGAGGTGGAGCACGAAGACC	CGAAGACC 1611
ОÞ	199 TCATGATCTCCCGGACCCCTGAGGTCATGCGTGGTGGTGGTGGTGAGCCACGAGACC	CGAAGACC 258
λŏ	1612 CCGAGGTCCAGTTCAACTGGTACGTGGACGCGTGGAGGTGCATAATGCCAAGACAAAGC	SACAAAGC 1671
Ωp	259 CIGAGGTCAAGTTCAACTGGTACGGGGCGGGGGGGGGGGG	GACAAAGC 318
δ	1672 CACGGGAGGAGCAGTTCAACAGCACGTTCCGTGTGGGTCAGCGTCCTCACCGTTGTGCACC	TGTGCACC 1731
ΩP	319 CGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCACCGCGCCTCACCGTCCTGCACC	CCTGCACC 378
ò	1732 AGGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCC	CCCAGCCC 1791
qq	379 AGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCCAACAAAAAAGCCCTCCCAGCCC	CCCAGCCC 438
ò	1792 CCATCGAGAAAACCATCTCCAAAACCAAAGGTGGGACCCGCGGGGTATGAGGGCCACATG	GCCACATG 1851
Ор	439 CCATCGAGAAAACCATCTCCAAAGCCAA	466
λŏ	1852 GACAGAGGCCGGCTCGGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTC	CCTCTGTC 1911
QQ	467	466
ò	1912 CCTACAGGCCAGCCCCGAGAACCACAGGTGTACACCCCTGCCCCCATCCCGGGAGGAGATG	AGGAGATG 1971
οg	467AGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCATCCCGG	ATGAGCTG 521
٥٠	1972 ACCAAGAACCAGGTCAGCCTGACCTGGTCAAAGGCTTCTACCCCAGCGACATCGCC	ACATCGCC 2031
qq	522 ACCAAGAACCAGGTCAGCCTGACCTGGTCAAAGGCTTCTATCCCAGGGACATCGCC	ACATCGCC 581
ò	2032 GIGGAGIGGGAGCAAIGGGCAGCCGGAGAACAACIACAAGACCACACCTCCCAIGCIG	CCATGCTG 2091
qq	582 GTGGAGTGGGAGAATGGGCAGCCGGAGAAACAACAACAACACCACGCCTCCCGTGCTG	CCGTGCTG 641
ò	2092 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG	GGTGGCAG 2151
QQ	642 GACTCCGACGGCTCCTTCCTTCTACAGCAAGCTCACCGTGGACAAGAGCA	GGTGGCAG 701
ò	2152 CAGGGGAACGICITCICAIGCICCGIGAIGCAIGAGGCICIGCACAACCACTACACGCAG	ACACGCAG 2211
QQ	702 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCATTACACGCAG	ACACGCAG 761
δ	2212 AAGAGCCTCTCCCTGTCCCCGGGTAAATGA 2241	
ପ ୍ର	762 AAGAGCCTCTCCCTGTCTCCGGGTAAATGA 791	

Search completed: July 18, 2003, 09:26:02 Job time : 3905.3 secs

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July 18, 2003, 04:14:58; Search time 583.029 Seconds (without alignments) 8686.944 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMAKIES	Query ce Match Length DB ID Description	30910	22	13 AAQ25443	18 AAT60739	22 AAF55225	24 ABK85577	723 18 AAT78802 Gamma heavy chain	7991CZ44 0C
	ength	2560	3223	2287	2287	4694	4694	4723	4723
مه	Query Match L	80.2	78.3	77.3	77.2	72.8	72.8	71.7	7 17
	Score	1804	1761.2	1739.4	1736.2	1638	1638	1611.8	1611 8
	Result No.		73	m	4	5	9	7	α

Human Igggammal he plasmid pCG7-96 nu pBAG101 insert. S Humanised anti-CD1 Encodes CD4-IgG2 chimeric Coding sequence fo CD4-IgG2 chimeric DNA encoding the h CD4-IgG2 chimeric Human death domain Sequence of a gene DNA encoding CD4-I Human fusion prote DNA sequence encod Human immunoglobul 2A2 human G2/G4 ch SEQ ID No. 5 that Human IgG CH1-hing Human IgG CH1-hing Human IgG CH1-hing Humanised anti-Fas	human/Fabbar Cgamm Anti-Fas humanised DNA encoding human Humanised HFE7A de Humanised anti-Fas Humanised anti-Fas Humanised anti-Fas Humanised anti-Fas
ABK85576 AAV39243 AAQ30903 AAQ55003 AAQ56003 AAQ58856 AAF77330 AAAF77330 AAAF77330 AAAF6891 AAAB50660 AAAF6661 AAAF6661 AAAF661 AAAF6661 AAAF62033 AAAF62033 AAT62937 AAAF66601	2007 2007 2007 2007 2007 2007 2007
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60000000000000000000000000000000000000	1459.8 1458.6 1458.6 1458.6 1458.6 1455.4 1455.4
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ALIGNMENTS

RESULT 1

Vector; pWDR1002; NotI; HindIII; pWDR1001; pSAB132; pBAG101; E. coli; JA231(Iq); ampicillin; resistance; immunoglobulin; signal sequence; humanised; SAB; heavy chain; variable; region; HV; 19G4; constant; HC; antibody; homolog; CD4; gp120; cell surface glycoprotein; CD4+; lymphocytes; helper; inducer; HIV; syncytia; formation; ss. /*tag= a 12..68 /*tag= b //tote= "Immunoglobulin signal sequence" 69..2296 /*tag= c pMDR1002 insert; pre-5A8 humanised heavy chain. Location/Qualifiers 12..2299 AAQ30910 standard; DNA; 2560 BP. 12..435 /*tag= d /number= 1 436..711 /*tag= e (first entry) /number= Homo sapiens 02-APR-1993 sig_peptide mat_peptide AAQ30910; intron exon Key AAQ30910 ~

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                                                      CCAGGICCAGCIGGAGICIGGGGCIGAGGIGAAGAAGCCIGGGAGCICAGIGAAGGI 127
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                                                                     GICCTGCAAAGCTTCCGGCTACACTTCACTGATTATGCTATACAGTGGGTGAGACACAGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents the insert of the vector pWDR1002. Three fragments were used in the construction of pWDR1002, a 443 bp Not! I fragment were used in the construction of pWDR1002, a 443 bp Not! I linearised pSAB112 (see AAQ30906). These fragments were ligated together and the ligation (see AAQ30909). These fragments were ligated together and the ligation resistance. The insert encodes the immunoglobulin signal sequence, amino acids (AA) 1-122 of the humanised SAB heavy chain, is: the constant region (HV) and AA114-AA478 of the human 1gG4 heavy chain, is: the constant region (HC). The polypeptide encoded by this sequence is an antibody homolog which was shown to bind to CD4 but did not block the binding of gpl20 to CD4. CD4 is a cell surface glycoprotein of induced syncytia formation. This homolog can be used in the constant prophylaxis and treatment of diseases caused by infective constant whose primary targets are CD4+ cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New anti-CD4 antibody homolognes - which bind CD4, do not b
binding of HIV gpl20 to CD4 but block HIV-induced syncytia
formation between CD4+ cells
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                                                                                                                                                                                                                   / number= 1
/ number= 4
/ note= "Human genomic IgG4 HC"
/ *tag= k
/ number= 4
1977..236
/ number= 1
/ number= "Human genomic IgG4 HC" -
/ 5.434
/ note= "Human genomic IgG4 HC" -
/ *tag= m/ note= "AA1-AA122 of humanised 5A8 VH'
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/*teg= h

/number= 3

/note= "Human genomic IgG4 HC"

1432..1549

/*teg= i

/number= 3

/*teg= j

/*teg= j
712..1005
*tag= f
/number= 2
/note= "Human genomic IgG4 HC"
1006..1395
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'number= 2
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P-PSDB; AAR28808.
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2165 TTCTTCCTCTACAGCAGGCTAACCGTGGACAAGAGCAGGTGGCAGGAGGGGAATGTCTTC 2224
                                                                                                                                                                                                                              Monoclonal antibody; Hu266; nootropic; neuroprotective; Abeta peptide; Alzheimer's disease; Down's syndrome; cerebral amyloid angiopathy; heavy chain; ds; gene therapy.
                                   TCATGCTCCGTGATGCATGAGGCTCTGCACAACACTACACACAGAAGAGCCTCTCCCTG
                        TCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTG
                                                                                                                                                                                                           encoding Humanised monoclonal antibody Hu266, heavy chain.
                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
12..2235
12..2235
12..236
12..68
12..68
7.tag= b
6..2232
7.tag= c
                                                                              TCCCCGGGTAATGAGTG 2244
                                                                                                                                            AAS11982 standard; DNA; 3223 BP.
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Homo sapiens.
Synthetic.
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CAGGCTGGGTGCCCCTACCCCAGGCCCTTCACACACACAGGGGCAGGTGCTTGGCTCAGACC
                                                                                       1206 CAGGCTGGATGCCCCTACCCCAGGCCCTGCGCATACA-GGGCAGGTGCTGCGCTCAGACC
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                                TGCCAAAAGCCATATCCGGGAGGACCCTGCCCTGACCTAAGCCGACCCAAAGGCCCAAA
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GCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGGGA 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The IgG1, in its nascent form, bears no sialy1-Lex side chains. The inventors designed a molecule including several such sites for attachment of sialy1-Lex side chains (see AAR2442, FT). The additional N-linked glycosylation sites are introduced at locations which impair complement fixing and Fc receptor binding ability. They are preferably located in the CH2 region of the Ig molecule. Antibodies bearing multiple sialy1-Lex determinants are useful for disrupting undesirable interactions between cells or proteins. Disrupting this interaction has therapeutic applications, for example, in minimising inflammation following tissue injury.
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                                                                                                                                                                                         Inhibition of cell adhesion mediated through ELAM-1 mol. bind:
- used in treating chronic inflammation, rheumatoid arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2287 BP; 483 A; 753 C; 652 G; 399 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1739.4;
Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                           Disclosure; Fig 1; 46pp; English.
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                                             90US-0618314.
               91WO-US08605
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Matches 2036; Conservative
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P-PSDB; AAR24442.
                                                                                                            Walz G;
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               18-NOV-1991;
                                            23-NOV-1990;
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                                            ACGGGAGGAGCAGTTCAACAGCACGTTCCGTGTGGGTCAGCGTCCTCACCGTTGTGCACCA
                                                                    1667 GCGGGAGGAGCAGTACAACAGCGCGTACCGTGTGGTCAGCGTCCTCACCGTCTGCACCA
                                                                                                         GGACTGGCTGAACGCCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCC
                                                                                                                                        1727 GGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCC
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                                                                                                                                                                                                                           The gene (AAT60739) encoding 1gG1 (AAW10550) can be subjected to sitedirected mutagenesis in order to introduce one or more N-linked glycan addition sites into the 1gG1 molecule (see also AAW10551). Eukaryotic host cells co-transfected with a vector carrying the the mutated 1gG1 gene and with a vector that expresses an alphatia. Stucosyltransferase capable of attaching sialy1-Le(x) groups at the glycosylation sites of the antibody molecule can be used in the prodn. of sialy1-Le(x)-modified antibody. Such an antibody has therapeutic applns, e.g. in minimising inflammation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAGTCCCAGGTGCAGCTGCTGCAGTCTGGGGCTGAGGTGAAGAAGAAGCCTGGGTCCTCGGTG
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                                                                                                                                                                                                                                                                                                                                                                                              decreasing extravasation-dependent organ damage and/or clotting
                                                                                                                            mol. - having
for protecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches 188; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2287 BP; 483 A; 758 C; 648 G; 398 T; 0 other;
                                                                                                                        P-selectin and opt. E-selectin binding organic sialyl-Le(x) and sulphated determinant, useful against inflammatory or immune reactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1736.2;
Pred. No. 0;
                                                                                                                                                                                               Disclosure; Page 40-41; 81pp; English.
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Best Local Similarity 88.9%;
Matches 2034; Conservative
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 GEN HOSPITAL
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TICTTCCTCTACAGCAGGCTAACCGTGGACAGAGGAGGGGAGGGGAAGAGTCTTC
                                                                    430 AACCICIAGAGCITICIGGGGCGAGCCGGGCCTGACITIGGCTTTGGGGCCAGGGAGTGGG
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human antibody display library; immune-related disorder;
immunomodulatory; IgGgamma4 heavy chain; pG4HE; cyclic;
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                                                                                                                                                                    A novel composition has been developed which comprises an immunoglobulin (1g) having an affinity constant (Ka) of at least 2 multiply.
100000000 M-1 for binding to a predetermined human antigen. The present sequence represents the kappa light chain plasmid pCMY-96 which includes the human gammal constant region and polyadamylation site. Anti-CD4 antibodies may be used in therapeutic and diagnostic applications, especially for the treatment of human diseases. These antibodies reduce activity of CD4 cells and reduce undesirable auctimmune reactions, inflammatory response and transplant rejection. Transpant and and activity of CD4 cells and reduce undesirable auctimmune reactions, undergoing isotype switching. These animals are produce a first is sorypes by undergoing isotype switching. These animals produce a first ig type that is necessary for antigen-stimulated B-cell maturation and can serious and produce one or more subsequent heterologous
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                                                                                                        transgenic mice - used in the
                                                                                                                                                                                                                                                                                                                                                                                Sequence 4723 BP; 1072 A; 1411 C; 1253 G; 987 T; 0 other;
                                                                                                                                                Example 42; Page 262-264; 396pp; English.
                                                                                                      Novel anti-CD4 antibody produced by tx
treatment of auto-immune disease etc.
10-OCT-1995; 95US-0544404.
                           (GENP-) GENPHARM INT INC.
                                                                               WPI; 1997-235888/21.
                                                    Lonberg N;
                                                                                                                                                                                                                                                                                                                                                          sotypes.
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The present sequence is used in the course of the specification. The specification describes a human antibodies which specifically bind to human cytocoxic T lymphocyte associated antigen-4 (CTLM-4). Such antibodies are used in methods for inducing, augmenting or prolonging an immune response to an antigen in a patient, where the antibodies are block binding of human CTLM-4 to human B7 ligands. The antibodies are also useful for treating autoimmune disease in a subject caused or exacerbated by increased activity of T cells and for treating prostate cancer, melanoma or epithelial cancer. A polyvalent or polyclonal antibody preparation comprising two antibodies of the invention are useful for suppressing a immune response in a patient. They are used for treating cancer, infectious diseases and promoting beneficial autoimmune reactions for the treatment of diseases with inflammatory or allergic components. The polyvalent or polyclonal preparations are useful for treating autoimmune diseases such as rheumatoid arthritis, myasthenia gravis and lupus erythematosus, multiple sclerosis, insulin-dependent contents.
                                                                                                                                                                                                                              Novel human sequence antibody that binds to human cytotoxic T lymphocyte associated antigen-4, useful for inducing, augmenting prolonging immune response to antigen or for suppressing immune response in patient
                                                                                                                                                                                                                                                                                                                                             Example 10; Page 93-94; 127pp; English
  24-AUG-2000; 2000WO-US23356
                                                                                    (MEDA-) MEDAREX INC
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                                                            1142 TCTCCCGGACCCCTGAGGTCACATGCGTGGTGGAGCGTGAGCCACGAAGACCTGAGG
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                              Length 4723;
Sequence 4723 BP; 1072 A; 1411 C; 1253 G; 987 T; 0 other;
                           Query Match 71.7%; Score 1611.8; DB 22; Lengt
Best Local Similarity 94.3%; Pred. No. 1.7e-313;
Matches 1722; Conservative 0; Mismatches 87; Indels
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Complementarity determining region, CDR; immune response; antibody; cytotoxic T lymphocyte associated antigen-4; CTLA-4; B7 ligand; cancer; autoimmune disease; inflectious disease; inflammation; allergy; rheumatoid arthritis; myasthenia gravis; lupus erythematosus; multiple sclerosis; insulin-dependent diabetes mellitus; inflammation;

Nucleotide sequence of pCG7-96.

(first entry)

29-MAY-2001

AAF55224;

ВР

AAF55224 standard; DNA; 4723

transplant rejection; graft versus host disease; ss

WO200114424-A2 Unidentified

01-MAR-2001.

14	
Page	GAG 2037
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	GCTTCTACCCCAGCGACATCGCCGT GCTTCTACCCAGCGACATCGCCCGT CAAGACCACACCCCCTCCCTGCTCGCA CAAGACCACACCCCCCTCCCTGCTCGCACAC CAGACCACACCCCCCTCCCTGCTCGCACAC [
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Pred. No. 1.7e-313;
0; Mismatches 87; Indels
 expression vectors for human IgG
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The plasmid is used in the construction of minigenes for expression of includes the human gammal constant constant and secretically a pecification describes transgenic non-human animals, especially a mouse, which are capable of producing a human heterologous antibodies of multiple isotypes by undergoing isotype switching. The transgenic animals havy and light chain transgenes are capable of functionally rearranging a heterologous diversity (D) gene in a heavy chain transgene comprising at least one V, D and J gene segment, and one constant region gene segment. The immunoglobulin (Ig) light chain cransgene comprises at least one V and J gene segment, and one constant region gene segment. The immunoglobulin (Ig) light chain cransgene comprises at least one V and J gene segment, and one constant region gene segment and one constant regions are used to revent efflux of neutrophils from animal. The antibody can be used to prevent efflux of neutrophils from antibodies are used to refation of transplanted organs. The antibodies can reduce undesirable autoimmune reactions, inflammatory responses and rejection of transplanted organs. The antibodies can reduce tissue damage and prolong survival in animal models of acute adult respiratory distress syndrome (ARDS) and anti-IL-8 antibodies can also be used for a asthma) and cystic fibrosis.
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acid induced lung injury, acute adult respiratory distress syndrome, ARDS; vasculitis; septic shock; allergic reaction; asthma; cystic fibrosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 71.6%; Score 1610.2; DB 19; Length 4723; Best Local Similarity 94.2%; Pred. No. 3.6e-313; Matches 1721; Conservative 0; Mismatches 88; Indels 18; G
                                                                                                                                                                                                                                                                                                                                                          Hybridoma producing antibody specific for interleukin-8 - used prevent efflux of neutrophils from vasculature, and treat reperfusion injury
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4723 BP; 1072 A; 1410 C; 1253 G; 988 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                               Example 42; Pages 312-315; 452pp; English.
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pBAG101 was designed to carry genomic DNA encoding the human IgG4 heavy chain constant region. The IgG4 DNA was isolated by polymerase chain reaction from human placental DNA using the primer sequences given in AAQ30907-08. The amplification product of this reaction was approx. 2109 bp. This fragment was inserted into EcoRS linearised pNN03 (see also AAQ3056) to give the intermediate plasmid pBAG101.
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                                                                                                                  71.6%; Score 1609.2; DB 13; Lengt 94.5%; Pred. No. 5.1e-313; . . . . . . . . . . . . . . . . . Indels ive 0; Mismatches 93; Indels
                                                                                           Sequence 2029 BP; 423 A; 710 C; 564 G; 331 T; 1 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Primer, polymerase chain reaction, amplify, IgG4, heavy chain, constant region, human, placenta, EcoR5, pNN03, pBAG101, HIV, antibody, anti-CD4, gp120, ss.
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binding of HIV gp120 to CD4 but block HIV-induced syncytia
formation between CD4+ cells
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                                                                                                                                                This sequence encodes a CD4-gamma2 chimeric heavy chain homodimer.

0.7 kb fragment, and cloned into M13mp18 forming M13mp18 (CD4). This was linearised with Pst1, and the SacII(flush) Pst1 fragment from Dbr gamma2 containing human gamma2 heavy chain (CH1 excn) isolated and ligated to the M13mp18 (CD4) vector. Resulting recombinants were then Streened by restriction analysis for the presence of both CD4 and CH1 which occur in trandem CD4 (EcoRI/Stu1) -CH1 (SacI (flush)/Pst1). CH1 which occur in trandem CD4 (EcoRI/Stu1) -CH1 (SacI (flush)/Pst1). CH1 which occur in trandem CD4 (EcoRI/Stu1) -CH1 (SacI (flush)/Pst1). CH1 heavy chain sequences in frame. The resulting chimeric DNA to the CH1 domain of heavy chain, plaques containing the V1V2 domains of CD4 fused with the correct sequence were then grown in Td1 cells and Rf DNA isolated from the cells.
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                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 99.7%; Score 1584.6; DB 13; Length 2482;
Matches 1587; Conservative 0; Mismatches 4; Indels 0; C
                                                                                                                                                                                                                                                                                      Sequence 2482 BP; 559 A; 812 C; 676 G; 435 T; 0 other;
                                                                                                                                  Claim 13; Fig 4; 90pp; English.
                             91US-0653684.
                                            (PROG-) PROGENICS PHARM INC.
            92WO-US01143
                                                               GA, Maddon PJ;
                                                                               WPI; 1992-300034/36.
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This sequence represents the CD4-IgG2 chimeric heavy chain nucleotide sequence from the CD4-IgG2 chimeric heterotetramer. The invention relates to an immunoconjugate comprising a cytotoxic radionuclide and a heterotetramer of two heavy chains and two light chains. The cytotoxic radionuclide is linked to either the heavy chains or the light chains, or considerable of the constant of the heavy chains are chimeric CD4-Ig (immunoglobulin) G2 chains encoded by cector CD4-kappa chains are chimeric CD4-kappa chains are con-polymorphic cells surface glycoprotein that is expressed on the surface of helper T lymphocytes, cells of the monocyte/macrophage lineage and dendritic cells. CD4 associates with major histocompatibility complex mediate efficient cellular immune response interactions. In humans CD4 is the target of interaction with the human immunodeficiency virus HIV. The immunoconjugate is used to kill cells infected with HIV, and for treating conservation in the immunoconjugate is used to diffection, and for assessing efficiency of treatments). The immunoconjugate is also used to determine the HIV consequence in the response in the surface of the inference of envelope glycoprotein burden, once determined, this information is used in the result of the consequence of the consequenc
                                                                                                                                                                                                                                                           CD4-1gG2 chimeric heavy chain heterotetramer; immunoconjugate; treatment; cytotoxic radionuclide; cell surface glycoprotein; prevent; infection; cellular immune response interaction mediator; HIV interaction; staging; prognosis; envelope glycoprotein burden; human; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CD4-19120 interaction is essential for infection). The heterotetramers are assembled intracellularly and secreted efficiently from mammalian cells, allowing high recovery and purification from the culture medium. They have longer half-life in serum and greater avidity than heavy chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New immunoconjugate, used to treat, prevent or image human immune deficiency virus infection, comprises radionuclide attached to heterotetramer of CD4-immunoglobulin chimeras
                                                                                                                                                                                                               CD4-1gG2 chimeric heterotetramer heavy chain nucleotide sequence.
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                                                      AAZ98856 standard; cDNA; 2482 BP
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93WO-US07422.
95US-0379516.
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P-PSDB; AAY85080.
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Score 1584.6; DB 21; Length 2482; Pred. No. 4.4e-308;

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Query Match Best Local Similarity

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ALIGNMENTS

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GENERAL INFORMATION:

APPLICANT: CO, MAN SUNG

APPLICANT: CARRENO, BEATRIZ

APPLICANT: CARRENO, BEATRIZ

APPLICANT: CALLINS, MARY

APPLICANT: GOLDMAN, SAWIEL

APPLICANT: GOLDMAN, SAWIEL
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2041 GAGAGCAATGGGCAGCGGAGAACTACAAGACCACCCCATGCTGGACT	2101 GGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGGAAC 	2161 GTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGACCTC	2221 TCCCTGTCCCCGGGTAAATGAGTGAATTC 2249 	55-	, Application US/10047542 No. US20020168367A1 SRMATION: LARRICK, JAMES W.	APPLICANT: WYCOFF, KEITH L. IIITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING IITLE OF INVENTION: AND BACTERIAL DISEASES FILE REFERENCE: 030905.0004.CIPI	PLLCATION NUMBER: US/10/047,542 LING DATE: 2001-10-26 LICATION NUMBER: PCT/US01/13932 NG DATE: 2001-04-28	RIOR APPLICATION NUMBER: 60/200,298 PRIOR FILING DATE: 2000-04-28 UNMBER OF SEQ ID NOS: 1.01 OFTWARE: Patentin Ver. 2.1	10 NO 55 TERGTH: 2009 TYPE: DNA ORGANISM: Homo sapiens	79.5%; Score 1787.6; DB 15; Length 99.7%; Pred. No. 0;	Vacive GGGCGAGCC - - - - - -	499 GGCAGGTGGCCCCAGCCAGGTGCACACCCCATGCCCGTGAGCCCCAGACCCTGCCCTGCCCTGCCCTGCCCTGCCCTGCCCTGCCCTGCCCTGCCCTGCCCTGCCCTGCCCTGCCCTGCCTGCCTGCCTGCCTGCCTGCCTGCCTGCCTGCCTGCCTGCCTGCCTGCTG	SCRAGGIGGCCCCCAGCCAGGIGCACACCCAGIGGCCCCGGGGCCCCAGACACTIGGCCCTGCCGGGCCCTGGGGCCCTCGGGCCCAGGCCCAGCTCTGCGCCCAGGCCCAGGCCTGCGGCCCTCTGCGCCCAGGCCCTGCGCCCAGGCCCTGCGGCCCAGGCCTGCGGCCCAGGCCTGCGCCAGGCCTGCGCCAGGCCCTGCGGCCCAGGCCCTGCGCCAGGCCCTGCCAGGCCCAGGCCCTGCCAGCCCAGGCCCAGCCCAGGCCCAGGCCCAGGCCCAGCCCAGGCCCAGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCAGGCCAGGCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCAGGCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCAGGCCAGGCCAGGCCCAGGCCCAGGCCCAGGCCCCAGGCCAGGCCCAGGCCCAGGCCAGGCCAGGCCAGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCCCAGGCCAGGCCAGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGCAG	619 CCACACCGCCGTCACATGCACCACCTCTTGCACCTCTGCGCCCACCGCCCATCGCTCTTGCACCTCCACCTCCACCCATCGCTCTTGCACCTCCACCTCCACCCATCGCTCTTGCACCTCCACCATCGCTCTTGCACCTCCACCATCGCTCTTGCACCTCCACCATCGCTCTTGCACCTCCACCATCGCTCTTGCACCTCTTGCACCTCCACCATCGCTCTTGCACCATCGCTCTTGCACCATCGCTCTCACATCAT	180 CCACACCGGGGTCACCACCACCACCTTGCAGCCTCCAAGGGCCCTTCGGTCT 679 TCCCCCTGGGCGCCTCCAGGAGCACCTCCGAGAGCACAAGGGCCCTGGGCTGCCTGG 740 TCCCCTGGGCGCCTCAGAGAGAACAAACAAACACAACCGCCTGGGCTTGTTTTTTTT	739 TCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCTCTGACC 300 TCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCTCTGACC 300 TCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCTCTGACC	799 GCGIGCACACTICCCAGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGG

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430 AACCICTAGAGCTTICTGGGGCGAGCCGGGCCTGACTTIGGCTTTGGGGCAGGGAGTGGG	610 AGCTCTGCCCACACGCGGGGCCCACACGCCCCTTGCCCCTGGGCCCCCTGGGCCCCCTGGGCCCCTGGGCCCCTGGGGCCCCTGGGGCCCCTGGGGGCCCCTGGGGGCCCCTGGGGGCCCCTGGGGGCCCTGGGGGCCCTGGGGGCCCCTGGGGGCCCCTGGGGGCCCCTGGGGGCCCCTGGGGGCCCCTGGGGGG	Db	Qy 730 GCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCTC 789	Oy 790 TGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCA 849	Qy 850 GCAGGGTGGTGACCTGCCTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAG 909 Db 423 GCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCTACATCTGCAACGTGA 482	OY 910 ATCACAGCCCCGCCAGCACCAGGTGGACAGGCGAGGTGGGGGGGG	QY 970 GGAGGGTGTCTGCTGGAAGCCAGGCTCAGCCTCCTGCCTG	Qy . 1030 GCCCCAGCCCAGGCAGCAACGCACACCCCATCTGTCTCCTCACCCCGGAGGCCTCTGCCC 1089 Db 603 GCCCCAGTCCAGGCAGCAGCCCCGTCTGCCTCTTCACCCGGAGGCCTCTGCCC 662	Oy 1090 GCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCCACCAGGCTCCAGGCAGCA 1149	Qy 1150 CAGGCTGGGTGCCCCTACCCCAGGCCCTTCACACACAGGGGCAGGTGCTTGGCTCACACC 1209	Oy 1210 TGCCAAAAGCCATATCCGGAAGACCCTGCCCTGACCTAAGCCGACCCCAAAGGCCAAA 1269	Oy 1270 CTGTCCACTCCCTCAGCTCGGACACCTTCTCTCCCCCAGATCCGAGTAACTCCCAATCT 1329	Oy 1330 TCTCTCTGCAGAGCGCAAATGTTGTGTCGAGTGCCCACGTGCCCAGGTAA 1380	Qy 1381 GCCAGCCCAGGCCTCCAGGTCGGACAGGTGCCCTAGAGTAGCCTGCAT 1440 Db 962 GCCAGCCCAGGCCTCCAGCTCAAGGCGGGACAGGTGCCTTAGAGTAGCCTGCAT 1021	OY 1441 CCAGGGACAGGCCCCAGCTGACACGTCCACCACCTCCATCTTCCTCAGCACC 1498 DD 1022 CCAGGGACAGCCCCAGCCGGGTGCTGACCTCCATCCTTCCT
CCTCACCGTTGTGCACCAGGACTGGCTGAACGGCAAGGAGT [[1816 CCARAGGGGGCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	DS 143B TCTGCCCTGGGGGGTGTGCCAACCTCTGTCCCTACAGGGCAGCCCCGAAGGCA 1497 Qy 1936 CAGGTTCACCCCCACCCCACGGGGGGGGGGAGGAGAACACAAGAACAAGAACAGGTTCACCTGACC 1995 DD 149B CAGGTTACACCTGCCCCATCCCAGGAGGAGAAGAACAACAAGAACAAGCTGGCTCAGCTGCCCCATCCCAGGAGAAGAAGAACAAGAACAAGAACAAGCTGAGCTGACCAAGAACAAC	Qy 1996 TGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGGAGCCAATGGGCAG 2055 Db 1558 TGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAATGGGCAG 1617	OY 2056 CCGGAGAACAACTACAAGACCACACCTCCCATGCTGGACTCCGACGGCTCCTTCTTCCTC 2115	QY 2116 TACAGCAAGCTCACCGTGGACAAGAGCAGGCAGCAGGGGAACGTCTTCTCATGCTCC 2175	Qy 2176 GTGATGCATGTGCACAACCACTACACGCAGAAGACCTCTCCCTGTCCCGGGT 2235 Db 1738 GTGATGCATGAGGCTCTGCACAACCACTACACACAGAAGAGCCTCTCCCTGTCTCTGGGT 1797	Oy 2236 AAATGAGTG 2244	RESULT 5 US-10-000-433-2	20.	; APPLICANT: 1810ad, 1840 ; APPLICANT: Lonberg, Nils ; APPLICANT: Halk, Ed ; TITLE OF INTENTION: TRANSCHIC TRANSCHROMOSOMAL RODENTS FOR MAKING HUMAN	FILE DEFERENCE: 014643-012110US CURRENT APPLICATION NUMBER: US/10/000,433 CURRENT APPLICATION NUMBER: US/10/000,433	FRIOR FILING DATE: 2000-11-30 NUMBER OF SEQ ID NOS: 10 SOFTWARE: Patentin Ver. 2.1	; SEQ 1D NO 2 ; TYPE: DNA 7723 ; TYPE: DNA 6724 Sequence	; OTHER INFORMATION: Description of Artificial Sequence: Gammal heavy; OTHER INFORMATION: chain plasmid; OTHER INFORMATION: pCG7-96	Query M Best Lo Matches

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APPLICATION NUMBER: US/08/485,163
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 37690-II-1-PCT-US
TELEOWMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEPAX: (212) 391-0525
                                                                                                                                                                                                                                                                                                                                                                                                           Score 1584.6;
Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                             70.5%;
99.7%;
                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 2482 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 99.7
Matches 1587; Conservative
                                                                                                                                                                                                                                                                                                                                         homo sapien
                                                                                                                                                                                                                                                                                                                                                         CELL TYPE: lymphocyte
                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                  unknown
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                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                       ORGANISM:
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US-08-485-163-4
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 1082 AACTCCTGGGGGGACCGTCAGTCTTCCTCTCCCCCAAAACCCAAGGACACCCTCATGA
                                                          TCTCCCGGACCCCTGAGGTCACATGCGTGGAGGTGGACGTGGACCACGAGGCCCCTGAGG
                                                                                                        1618 TCCAGTTCAACTGGTACGTGGACGCGTGGAGGTGCATAATGCCAAGACAAAGCCACGGG
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                                    1558 TCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGACGTGAGCCCACGAAGACCCCCGAGG
                                                                                                                                                                          AGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAGGACT
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; Publication No. US20020098191A1
; GENERAL INFORMATION:
   APPLICANT: Beaudry, Gary A.
   APPLICANT: Maddon, Paul J.
   TITLE OF INVENTION: CD4-GAMMA2 CD4-IgG2 CHIMERAS
   NUMBER OF SEQUENCES: 10
   CORRESPONDENCE ADDRESS:
   ADDRESSEE: Cooper & Dunham Lip
   STREET: 1185 Avenue of the Americas
   CITY: New York
   STATE: New York
   STATE: New York
   STATE: 10036
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-485-163-4
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1344 CAGETAMATCCANCTCTCCACCTCCACCTCACCTCACCTCACCT	CURRENT APPLICATION NUMBER: US/09/766,995 CURRENT FILING DATE: 2001-01-22 NUMBER OF SEQ ID NOS: 9 SEQ ID NO 3 3 SEQ ID NO 3 3 LENGTH: 2402 TYPE: DNA TYPE: DNA ONGANISM: Homo sapiens	Watches 1587; Conservative . 0; Mismatches 4; Indels 0; Matches 1587; Conservative . 0; Mismatches 4; Indels 0; 654 GCCTCCACCAAGGGCCCATGGTTTCCCCCTGGGGCCCTGCTCCAGGAGGCCAGGGGGGGG	Dy 714 AGCACAGCGCCTGGGCTGCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCG 773 Db 748 AGCACCCCTGGGCTGCTGCTCAAGGACTACTTCCCCGAACCGGTGTCG 807 Dy 774 TGGAACTCAGGGGGTGACACCTCCCCAGCTGTCCTCG 833	808 TGGAALTCAGGCGCTCTGACCAGCGGTGTACATCTTCCCAGCTGTCCTTACAGTCCTTACAGTCCTTAGGGTGTCCTTAGGGTGTCCTTAGGGTGTCCTCAGGGGTGTCCTCAGGGACCTTCGGCACCCAGACCCAGACCCAGACCCAGACCCAGACCCAGACCCAGACCCAGACCCAGACCCAGGGGTGGTGACCGTGGCCCTCCAGGGAACTTCGGCCACAGAACCTTCGGCAGACCCAGAACCTTCGGCACCCAGAACCAGAACTTCGGCAACCTAGAGCAGCAGCAGAACCTTCGGCACCCAGAACCAGAACTTCGGCAACCTAGAACCAGAACTTCGAGCAACCAGAACCAGAACCTAGAACCAGAACCTAGAACCAGAACTTCGGCACCCAGAACACAGAACCAGAACCAGAACCAGAACCAGAACCAGAACCAGAACCAGAACCAGAACCAGAACCAGAACCAGAACCAGAACCAGAACCAGAACCAGAACCAGAACCAGAACCAGAACAAC	0y 894 TACACCTGCAACGTGGTGACAAGACCAAGGTGGACAAAACAGTTGGTGAG 953 1	1014 GCACCCGGGCTGTGCAGCCCCAGGCCAGGCAAGGCAGGCCCCATCTGTCTCTCTC	1074 CCGAGGCCTCTCGCCCCACTCATCAGGGGGAGAGGGCTTTTTTCCACC 1108 CCGAAGGCCTCTGCCCGCCCCACTCATGCTCAGGGAGAGGTCTTCTGGCTTTTTTCCACC 1134 AGGCTCCAGGCAGGCAGGGGGGGGGGGCCTTCAGAGGCTTTTTCCACC 1134 AGGCTCCAGGCAGGCTGGGTGCCCCTACCCCAGGCCCTTCACACACA	1168 1194 1228	1254 GACCCCAAAGGCCAAACTGTCCACTCGCTCGGACACCTTCTCTCCTCCCAGATCC 1288 GACCCCAAAGGCCAAACTGTCCACTCGGCTCGGACCTTCTTCTCTCCTCCAGATCC	Oy 1314 CAGTAATCCCAATCTTCTCTGCAGAGGGAATGTTGTGTGGGTGCCCACGGTGCC 1378 Db 1348 GAGTAACTCCCAATCTTCTCTCTGCAGAGGGCAAATGTTGTGTGTG	1408 1468	OY 1494 GCACCACCTGCGGCAGCACCACCATCATCTTCTCTCCCCCCAAAACCCAAGGACACCCTC 1553
—	1407 ; C C C C C C C C C C C C C C C C C C	C 1553 Bee C 1587 Aa Oy C 1613 Db				TCTGTCC 1947 GAGATGAC 1973	ATCGCCGT 2033 [CATCGCCGT 2067	CATGCTGGA STGGCAGCA IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	And Coda 2213	224	Cation US/09766995 Oy 0052481A1 OY OY 0052481A1 OY	CD4-GAMMA2 AND CD4-IgG2

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-23.rnpo		410 CI 712 A 470 P	COTGGAACTCAGGGGGCTCTGAACTCGGGGACCCTCCAGCAACTCCGTCAGGAGGGGGGGG	H - 11-0	1012 ACGCACCCGGGTGTTTTTCCA 113	830 AC 1132 C 890 C	52 G	1312 CCGAGTAACCCCATAGAT CTGCACACACCACCACACACGCGGGACACGCGCGGACACACTAGAT 118 1372 CCGAGGTAACCCAGGCCCAGGCCTCCAGCTCAAGGCGGGGACACCCTAGAGT 118 1332 CCCAGGTAACCCAGGCCCAGGCCTCCAGCTCAAGGCGGCACCCTCCATCCTTCCT		1552 T 1310 T 1612 (2 CACGGGAGGAGTTCAACAGGACGTTCCG 	
us-09-627-896b	Sat Jul 19 10:01:52 2003	•	PAG OCI	DD 1708 CGGGANGSTON TO CGGGANGSTOLD THE THINK THE THE THINK THE THINK THE	1828 ATCGAGARAACCATCTCTCTCCCCTGGGAGTGGCGCTTTTTTTTTT	4 6 7	2034 GGRGTGGGRATGGGCAATGCTTTTTTTTTTTTTTTTTTTT	2128 CONTROLL OF THE CONTROLL	RESULT 8 RESULT 8 VS-10-153-382-2 VS-10-153-382-2 S Nop US2030086930A1 S SAQUENCE 2, Nop US2030086930A1 S SAUGHTON S S S S S S S S S S S S S S S S S S S	GENERAL INCORPTER PRODUCTS INC. APPLICANT: PETER PRODUCTS INC. TITLE OF INVENTION: 1025 OF ANTI-CTLA-4 ANII-CO- FILE REPERENCE: PC2-31048 CURRENT APPLICATION NUMBER: 60/293042 CURRENT FILING DATE: 2002-05-23 PRIOR APPLICATION NUMBER: 60/293042 CURRENT FILING DATE: 2001-05-23	NUMBER OF SEQ L. 2.1 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 3.5 IENGTH: 1999 TYPE: DNA Homo sapien8	0; Gaps

us-09-627-896b-23.rnpb	SEQUENCE CHAR. TYPE: nuc STRANDEDN TOPOLOST: SEQUENCE ITPE: US-10-027-075-29 Query Match	10 10 10 10 10 10 10 10
Oy 1732 AGGACTGGCTGAACGGCAAGGAGTACAAGTGCAAACAAAGAAGTACAAGTGCAAAAGAAGAAAGA	Oy 1792 CCATCGGCANGON	Db 1139 COMPUTED CONTRIBUTION CONTRIBUTION

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; TITLE OF INVENTION: AND BACTERIAL DISEASES; FILE REFERENCE: 030905.0004.CIP1
; CURRENT APPLICATION NUMBER: US/10/047,542
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: PCT/US01/13932
; PRIOR APPLICATION NUMBER: 60/200,298
; PRIOR APPLICATION NUMBER: 60/200,298
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                  Score 1547.2;
Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 94.1%;
Matches 1711; Conservative
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US-10-047-542-54
                                                                                                                                                                                      LENGTH: 2009
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KEITH L. .
NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL
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                                                                   TAAGCCAGCCCACGCCTCCAGCTCCAAGGCGGAAAGGTGCCCTAGAGTAGCCTG
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                                rcrrcrcrcradadcccaaarcrrdradadaaacrcacardcccaccardcccadd
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US-10-047-542-54
US-10-047-542-54
Sequence 54, Application US/10047542
Hublication No. US2020168367A1
GENERAL INFORMATION:
APPLICANT: LARRICK, JAMES W.
APPLICANT: WYCOFF, KEITH L.
TITLE OF INVENTION: NOVEL IMMUNOADHESI
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LENGTH: 2071

TYPE: DNA

ORGANISM: Artificial Sequence
ORGANISM: Artificial Sequence
OTHER INFORMATION: Description of Artificial Sequence: Designed DNA
OTHER INFORMATION: antibody the heavy chain of a humanized anti-Pas
FRATURE: OFFACTION: (21)...(77),
NAME/KEY: sig Peptide
FRATURE: OCATION: (21)...(77),
NAME/KEY: intron
FRATURE: (735)...(1125) APPLICANT: Seriawa, No. US20030103976Alufusa APPLICANT: Seriawa, No. US20030103976Alufusa APPLICANT: Naturama, No. US20030103976Alufusa APPLICANT: Tamakir, Kaori TTLECANT: Tamakir, Kaori TTLECANT: Tamakir, Tohur TTLE OF INVENTION: Tohur Tohur Tohur Tohur FILE OF INVENTION: APLICATION UNMERS: US/10/216,484 CURRENT APPLICATION UNMERS: US/10/216,484 PRIOR FILING DATE: 2002-09-09/216,484 PRIOR PRING DATE: 2000-02-09/216,484 PRIOR PRING DATE: 2000-02-09/216,484 PRIOR PRING DATE: 2000-02-09/216,484 PRIOR PRING DATE: 1298-04-01 US/10/215,883 LENGTH: 200 Sequence 116, Application US/10216484 Publication No. US20030103976A1 FEATURE FEATURE LOCATION (1619) ... (1715) FEATURE:
NAME/KEY: exon
LOCATION:
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NAME/KEY: exon
LOCATION:
NAME/KEY: exon
FEATURE:
FEATURE: FEATURE:
NAME/KEY:
LOCATION: (1126). (1170) NAME/KEY:
NAME/K NAME/KEY: exon LOCATION: (21)..(734) 770 ccatatecgggaggaccetgccetgacetaagcccaccccaaaggccaaactetli 1279 CCCTCAGGTCGGACGTTCTCCTCCGAGATCCGAGTAACTCCCAATCTTCTCTCTGG 1338 1339 AGAGGGAAATGTTGTGTGGG------TGCCGACGTGCCCGAGGTAAGCCAGGCCA 1389 1390 GGCCTCGAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCATCCAGGGACA 1449 950 GGCCTCGAGCTCAAGGCGGGACAGGTGCCCTAAGAGTAGCCTGCATCCAGGGACA 1009 1450 GGCCCAGGTGGTGAGACGTCCACTTCTTGTTGTTGTGAGACC---ACCTGCGG 1506 1010 GGCCCCAGCCGGGTGCTGACACGTCCACCTCCATCTTCTTCTGAGCACCTGAACTCCTGG 1069 1507 CAGCACCGTCAGTCTTCCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCCGGGA 1566 1070 GGGGACCGTCAGTCTTCCTTTCCCCCCAAAACCCAAGGACACCTCATGATCTTCCGGGA 1566 1567 CCCCTGAGGTCACGTGGTGGAGGTGGAGGTGAGCCACGAAGACCCCGAGGTCCAGTTCA 1626 1627 ACTOGTACGTGGACGGTGGAGGTGCATAATGCCAAGACAAAGCCACGGGAGGAGCAGT 1686 1190 ACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGGAGCAGAGTGCAAATGCCAAGACAAAGCCGCGGGAGGAGGAGCAGT 1249 1687 TCHACAGGACGTTCCGTGTGGTCAGCGTCCTCACGGTTGTGCACCAGGACTGGACTGAACG 1746 1250 ACAACAGCACGTGGTGGTCAGCGTCCTGCAGCAGCAGGGTGGCTGATG 1309 1747 GCAAGGAGTACAAGTGCAAGGAGCAAGAAGGGCGTCGCAGGCCCCATCGAGAAAGA 1806 1310 GCAAGGAGTACAAGTGCAAGGTCTCCAACAAGGCCCTCCCAGGCCCCCATCGAGAAAACCA 1369 1807 TCTCCAAAACCAAAGGTGGGACCCGCGGGGGTATGAGGGCCACATGGACAGAGGGGCGGCTC 1866 1370 TCTCCAAAGCCAAAGGTGGGACCGGTGGGGTGCGAGGGCCACATGGACAGAGGCCGGCTC 1429 1867 GGCCCACCCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCCTACAGGGAGCCC 1926 1430 dGCCCACCTCTGCCTGAGAGTGACCGCTGTACCAACCTCTGT-CCTACAGGGCAGCCC 1488 1987 AGCCTGACCTGGTCAAAGGCTTCTACCCCAGGGACATCGCCGTGGAGTGGAGGGG 2046 1609 AATGGGCAGCCGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGAGGGCTCC 1668 2047 APTGGGGGGGGGGGAGGAACTACAAGACCAAGCGACGCGGATGCTGGACTCGGAGGGGTGG 2106 à Dp DP ò DP $p_{\mathbf{p}}$ ò PP δ ОР

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.1%; Score 1463.4; DB 15; .2%; Pred. No. 0;	λ _ο qα	1028 CAGCCCCAGGCCAGGCCAGCCAGCCCCATCTGTCTCCTCACCCGGAGGCCTCTGC 1087
F F-	Š d	CGCCCCACTCATGCTCAGGAAGGGTCTTCTGGCTTTTTCCACCAGGCTCAGGGAGG 1
AAGGT 1	QQ ab	1148 CACAGGCTGGGTGCCCCTACCCCAGGCCCTTCACACAGGGGCAGGTGCTTGGCTCAGA 1207
GTCCTGCAAAGCTTCCGGCTACACATTCACTGATAATGCTATACAGTGGGTGAGACAGGCTACACAGGCTTCCGGCTACACATTATGCTATACAGTGGGTGAGACAGGCTACACACTGCTACACAGCTTCACAGGCTACAGGCTTCACAGGCTACAGGGTTCACAGGGGTAAAAAGAGGGTTACACAGATCACAGCTACAGGGTAAAAAAGAGGGTAAAAAAAGGGTTACAACAGGCTACACAGCTACACAGGGTAAAAAAAGGGTTACAACAGAGGGTTACACAGAGGGTTACAAAAAAGAGGGTTACAAAAAAGATACAAGAGGGTTACAAAAAAAA	QV Db	1208 CCTGCCAAAAGCCATATCCGGGAGGACCCTGCCCCTGACCTAAGCCGACCCCAAAGGCCA 1267
TCTGGACAGGCCTCGAGTGGATTGGAGTTATAATATTTACTATGATAATACAAACTA 24	Oy Og	1268 AACTGTCCACTCCGTCAGCTCGGACACCTTCTCTCCTCCCAGATCCGAGTAACTCCCAAT 1327
CAACCAGAAGTTTAAGGGCAAGGCCACAATGACTGTAGACAGTCGACGAGGCACAGCCTA 30 CAACCAGAAGTTTAAGGGCAAGGCCACAATGACTGTAGACAAGTCGACGAGGCACAGCCTA 30 CAACCAAAGTTCAAAGGCCAAATGAATGATTGAAAGATAAAAGTTCAAAAGTTCAAAGGCAAGCCTA 31	QQ Op	1328 CTTCTCTCTGCAGAGCGCAAATCTTGTGTCGAGTGCCCACGTGCCCAGGT 1378
TATGGAACTTAGTTCTTTGAGATCTGAGGATACGGCCGTTTATTACTGTGCAAGAGCGGCCGTTATTACTGTGCAAGAGCGGCCGTTATTACTGTGCAAGAGCGGCCGTTATTACTGTGCAAGAGCGGCCGTTATTACTGTGCAAGAGCGGCCGCTTATTACTGTGCAAGAACGCGCCGCCAAGAAAAAAAA	QQ Dp	1379 AAGCCAGCCCAGGCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCTGC 1438
CTGGTATATGGACTACTGGGGTCAAGGTACCCTTGTCACGGTCTCCTCAGGTGACTTAGGACTACTGGGGTCCTTGTCACGGTCTCCTCAGGTGAGTTCCTT	ζ qα	1439 ATCCAGGGACAGCCCCAGCTGCGTGACACGTCCACCTCCATCTTCCTCCAGCACC 1498
AAAACCTCTAGAGCTTTCTGGGGCGGGCCGGGCCTGACTTTGGCTTTGGGGCAGTG	Oy Dp	1499ACCTGCGGCAGCACCACCATCCTCCTCCTCCCCCAAACCCAAGGACACCTCAT 1555
TACTTCGATGTCTGGGGCGCAAGGGACCCTGG	λο O	1556 GATCTCCCGGACCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCCGA 1615
CTGGACCCTGCACCCTCGTGGATAGACAAGAACCGAGGGGCCTCTGCGCCCTGGGC		1616 GGTCCAGTTCAACTGGTACGTGGACGCGTGGAGGTGCATAATGCCAAGACAAAGCCACG 1675
CCAGCTCTGTCCCACACCGCGGTCACATGGCACCACCTCTTTGCAGCCTCCACACGG	o o	GGGGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAGAACAGAGCAGTAACAGCAGTACGTGTCAGCGTCCTCACCGTCTGCACCAGGA
	oy Ob	1736 CTGGCTGAACGCCAAGGGTACAAGTGCAAGGTCTCCAAAGGGCCTCCCAGCCCCAT 1795
CCCAICGGICTITCCCCTGGCACCCTCCAAGAGCACCTCTGGGGGGGAAGCGCCCT 51 GGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGTGTCGTGGAACTCAGGGGC 78 CCCTTGCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	Qy Dp	1796 CGAGAAAACCATCTCCAAAACCAAAGGTGGGACCCGCGGGGTATGAGGGCCACATGGACA 1855
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AGATCACAAGCCCAGCAACCAAGGTGGACAAGCTTGGTGGAGACCTACAGCTGGGAGGG 96	ço,	1976 AGAACCAGGTCAGCTGACCTGCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGG 2035
955 GAGICACAGCACCAGCAGCTGGACAAGGTGGACAGGTGGTGAGAGGCCAGCAGGG 754 968 AGGGAGGTGTCTGCTGGAAGCCAGGCTGAGCCCTCCTGCCTG	oy da	2036 AGTGGGAGGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGACT 2095

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LENGTH: 2077 TYPE: DNA	ò	188 TCCTGGACAGGGCCTCGAGTGGATTGGAGTTATTAATATTTACTATGATAATACAAACTA 247
oring Samuel Sequence Francis Sequence	qa	203 CCCTGGACAGGCCCTTGAGTGGAGAGATTCATCTTCTGATAGCTATACTAACTA
NAME/KEY: sig peptide LOCATION: (27)(83)	ò :	CAACCAGAAGTITAAGGGCAAGGCCACAATGACTGTAGACAAGTCGACGAGCACAGCCTA 3
NAME/KEY: intron measurino: (741)(1131)	~~~	36
FEATURE: NAME/KEY: intron LOCATION: (1177)(1294)	qo	
: intron : (1625)	ç qa	368 CTGGTATATGGACTACTGGGGTCAAGGTACCCTTGTCACCGTCTCCTCAGGTGAGTCCTT 427
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NAMB/KEY: exon NAMB/KEY: (1132)(1176)	g &	402IACTICGATGTCTGGGGCGAAGGGACCCTGGT
FEATURE: NAME/KEY: exon LOCATION: (1295)(1624)	qa	434 433
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	Qy	728 GGGCTGCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGC 787
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NAMEKKI: CDS LOCATION: (1722)(2042) PRATURE:	qa	701 GAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGGTGAGAGGCCAGCACCAGGGG 760
OTHER INFORMATION: Description of Artificial Sequence: Designed DNA CHER INFORMATION: encoding the heavy chain of humanized anti-Fas in THPORMATION: antibody US-10-216-484-156	& 8	968 AGGAGGGGTGTCTGCTGGAAGCCAGGCTCAGCCTCTGCTGGACGCACCCCGGCTGTG 1027
Query Match Query Match Best Local Similarity 81.9%; Pred. No. 0; Matches 1843; Conservative N. Mismatches 171: Indele 215. Gans 5.	ζό O	1028 CAGCCCCAGCCCAGGCAAGCAAGCCCATCTGTCTCCTCACCCGAAGCCTCTGC 1087
B CACCATGGGTTGGAACTGTATCATCTTTCTGGTTACCACAGCTACAGGTGTGCACC 67 23 CACCATGGGATGGAACTGTATCATCTTTCTGGTTACCACAGCTACAGGTGTGCACTC 67 23 CACCATGGGATGGAAGTTACATCTTTTTTTTTTTTATACAAGCTACAAGTTACATCTTCTTTTTTTATACAAGCTAACAAGTTACATCTTTTTTTT	Oy Dp	1088 CCGCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCCACCAGGGTCCAGGCAGG
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PREDICANT: GHISAGA PAPETICIA L.

PREDICANT: GHISAGA PAPETICAL

APPLICANT: ROSA, WOSERH J.

APPLICANT: ROSA, WOSERH J.

APPLICANT: ROSA, WOSERH J.

APPLICANT: ROSA, WOSERH J.

TITLE OF INVENTION:

NUMBER PROMATIVE PROPHILAXIS AND PREATHENT OF AIDS, ARC AND HIV INFECTION

TITLE OF INVENTION:

NUMBER PROGRAMMENT & MITCOFF, IID.

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	b se ggataactaccaccatattacttactatactcaccaccacca	Qy 410 CTCCTCAGGTGAGTCCTTAAA	Qy 435 CTAGAGCTTTCTGGGGCGGGGCCTGACTTTGGCTTTGGGGCAGGGAGGTGGG	490		Qy 550 GGACCTGGGACCCTGGTGGATAGACAAGAACCGAGGGCCTTGCGCCCTGGGCCCT	Qy 610 AGCTCTGTCCCACACGCGGTCACATGGCACCACCTCTTGCAGCGCCTCCACCAAGGGCCC ACAAGGGCCC 657 AGCTCTGTCCCACACGGGGTCATGGCACCACCACCACAGGGCC	Qy 670 CATCGGTCTTCCCCTGGCGCCCTGGTCCAGGAGCACCTCCGAGAGCACACGGGCCCTGG	Oy 730 GCTGCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGGGCGCTC	Oy 190 IGACCAGCGGGGGGGGGGGCGTGCAGCTGCTCCAGGACTCTACTCCTACAGTCCTCAGGACTCTACTCCCTAGTCCTACAGTCCTCAGGACTCTACTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTACTCCCTAACAGTCCTCAGGACTCTACTACTCCCTCAGGACTCTACTACTAGTCCTAACAGACTCTACTACTCCCTCA	Oy 850 GCAGCGTGGTGGTGCCCTCCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAG	QY 910 ATCACAACCCAGCAACAACACCAAGGTGGACAAGACAGTTGGTGAGAGGCCAGCTCAGGAG DD 1	QY 970 GGAGGCTGTCTGCTGGAGGCAGGCTCCTGCTCCTGGACGCACGC	ÓY 1030 GCCCCAGGCCAGCAAGGCAAGGCACCATCTGTCTCTCACCCGAAGGCTTTGCCC D	QY 1090 GCCCCACTCATGCTCAGGAGAGAGAGCTCTTCTGGCTTTTTCCACCAGGCTCCAGGCAGG	QY 1150 CAGGCTGGGTGCCCTACCCCAGGCCTTCACACACACACAGGGCAGGTGCTTGGCTCAGACC D	Oy 1210 TGCCAAAAGCCATATCCGGAAGACCCTGCCCCTGACCTAAGCCGACCCCAAAGGCCAAA	Qy 1270 CTGTCCACTCCGTCAGACACTTCTCTCCCCAGATCCGAGTAACTCCCAATCT	OY 1330 TCTCTGCAGAGCGCAAATGTTGTGTCGAGTGCCCACGTGCCCAGGTAAGCCAGGTAAGCCAGA
) MOLECULE TYPE: DNA (genomic); HYPOTHETICAL: NO ANTI-SENSE: NO	FEATURE: NAME/KEY: sig_peptide LOCATION: 12.68	NAME/KEY: mat_peptide 			; NAME/KEY: intron ; LOCATION: 14321549	FEATURE: NAME/KRY: intron LOCATION: 18801976	NAME/KEY: misc_feature 	EY: exon ON: 12435	; FEATURE: ; NAME/KEY: exon ; LOCATION: 7121005 ; FEATURE:		COCATION: 15501879 FEATURE: NAME/KEY: exon 	; FEATURE: ; NAME/KEY: CDS ; LOCATION: join(12435, 7121005, 13961431, 15501879, US-07-1508.44	80.2%; Score 1804; DB 2; Length 2560; larity 89.2%; Pred. No. 0;	COLISE VACING CCATGGGTTGGAACTGTATCA CATGGACTGGACTTGAGGC	68 CCAGGTCCAGCTGGTGCAGTCTGGGGTGAAGAAGCCTGGGAGCTCAGTGAAGGT	128	188 TCCTGGACAGGCCTCGAGTGGATTGGAGTTATTAATATTTACTATGATAATACAAACTA 160 CCTTGGACAGTGGATTGGAGTTATTAATATTTACTATGATAATACAAACTA 160 CCTTGCAACAGTGGATTGGAGTTATTAATATTTACTATGATAATACAAACTA	248 CAACCAGAAGTTTAAGGGCAAGGCCACAATGATGATGATGATGATGATGATGATGATGATGATGATG	

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                                                 COUNTRY: USA

COUNTRY: USA

COUNTRY: USA

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: TBM PC Compatible
COMPUTER: PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10043
FLING DATE: 14-JUN-1995
CLASSIFICATION STATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,213
FLING DATE: 14-JUN-1995
CLASSIFICATION NUMBER: LECH, RATEN F.
RIGHSTERATION NUMBER: B.
APPLICATION 
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89.1%; Pred. No. 0;
iive 0; Mismatches
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEFX: 200154
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 2287 base pairs
          225 Franklin Street
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STRANDEDNESS: single
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Matches 2038; Conserv
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                                                         GGCCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCATCCAGGGACA
                                                                                                                                                          GCCCCCAGCTGGGTGCTGACACGTCCACCTCCATCTTCCTCAGCACC---ACCTGCGG
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Sequence 8, Application PC/TUS9610043

GENERAL INFORMATION:
APPLICANT: THE General Hospital Corporation
TITLE OF INVENTION: P-SELECTIN LIGANDS AND RELATED MOLECULES
TITLE OF INVENTION: P-SELECTIN LIGANDS AND RELATED MOLECULES
TITLE OF INVENTION: AND METHODS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
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1578 ACGTGCGTGGTGGACCTGAAGCCCCGAAGGTCCAGTTCAACTGGTACGTG 1570	RESULT 3 US-08-480-036-1 I Sequence 1. Application US/08480036 Fetent No. 572363 GENERAL INFORMATION: APPLICANT: Seed, Brian et al. TITLE OF INVENTION: INHIBITION OF CELL ADHESION TITLE OF INVENTION: PROTEIN-CREBOHYDRATE TITLE OF INVENTION: PROTEIN-CREBOHYDRATE TITLE OF SEQUENCES: 4 NUMBER OF SEQUENCES: 4 NUMBER OF SEQUENCES: 4 CURRESPONDENCE ADDRESS: ADDRESSEE: Fish & Richardson STREET: 225 Franklin Street CITLE MOSION: STATE: Massachusetts COUNTRY: U.S.A. ZIP: 02110-2804 COMPUTER: IBM PS/2 Model 50Z or 55SX CURRENT APPLICATION DATA: CURRENT APPLICATION DATA:
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Pred. No. 0;
0; Mismatches 219; Indels
APPLICATION NUMBER: US/08/480,036
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION 1424:
APPLICATION NUMBER: US/07/618,314C
FILING DATE: No. 5723583ember 23, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/067001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-8906
TELEFAX: 200154
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHRARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73.48;
87.28;
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Best Local Similarity 87.2
Matches 1998; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   307 GCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      243 AACTACAACCAGAAGTTTAAGGGCAAGGCCACAATGACTGTAGACAAGTCGACGAGCACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             390 CAAGGTACCCTTGTCACCGTCTCAGGTGAGTCCTTAAAAACCTCTAGAGCTTTCTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 482 GCAGGCCTGACCTTGGCTTTGGGCCAGGGAGGGGGCTAAGGTGAGGCAGGTGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      630 TCACATGGCACCACCTCTTGCAGCCTCCACCAAGGGCCCCATCGGTCTTCCCCCTGGCG
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                                                                                                                                                                                                                                           Length 2287;
                                                                                                                                                                                                                                       Query Match 73.4%; Score 1651.6; DB 1; Length Best Local Similarity 87.2%; Pred. No. 0; Matches 1998; Conservative 0; Mismatches 219; Indels
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2287
                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                   linear
                                                                                                                                                       ; TOPOLOGY:
US-08-461-968A-1
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                              AAACCAAAGGTGGGACCCGCGGGGTATGAGGGCCACATGGACAGAGGCCGGCTCGGCCCA 1872
                                                                                                                                                   CCACAGGTGTACACCCTGCCCCCATCCCGGGAGAGATGACCAAGAACCAGGTCAGCCTG 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2025 ACCTGCCTGGTCAAAGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGTGGGAGAGGCAATGGG 2084
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   1753 AGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCATCGAGAAACCATCTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1993 ACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAATGGG
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APPLICANT:
Seed et al., Brian
TITLE OF INVENTION:
INHIBITION OF CELL ADHESION
TITLE OF INVENTION:
INHIBITION OF CELL ADHESION
TITLE OF INVENTION:
INHIBITION OF CELL ADHESION
CORRESPONDENCE ADDRESS:
ADDRESSE:
ADDRESSE:
ADDRESSE:
Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: BOSTON
STRATE: MA
COUNTRY: USA
ZIP: O210-2804
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER REDABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER REDABLE FORM:
MEDIUM TYPE: PLOPSY MS-DOS
SOFTANDE: PLOPON DATA:
APPLICATION NUMBER: US/08/461,968A
FILING DATE: 05-401-1995
CLASSIFICATION NUMBER: US 07/618,314
FILING DATE: 23-NOV-1995
ATTORIEY ASPLICATION NUMBER: US 07/618,314
FILING DATE: 23-NOV-1995
ATTORIEY AGENT INFORMATION:
NAME: Lech, Karen F.
REGISTRATION NUMBER: 35,238
REFERENCE DOCKET NUMBER: 35,238
REFERENCE DOCKET NUMBER: 35,238
REFERENCE OF ALT/542-8906
TELLEPAN: 617/542-8906
TELLEPAN: 200154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08461968A; Patent No. 5801044; GENERAL INFORMATION:
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US-08-461-968A-1
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	895 TCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAGAGCCCAGCAACACC 954	930 AAGGTGGACAGATGGTGAGAGGCCAGCTCAGGAAGGAAGG	990 CAGGCTCAGCCTCCTGCTGGACGCACCCGGCTGTGCAGCCCCAGCCCAGGCAGCAA 1049	1050 GGCAGGCCCCATCTCTCCTCACCCGGAGGCCTCTGCCCGCCC	1110 GAGGGTCTTCTGGCTTTTTCCACGGGCTCGGGCGCGCGCG	1170 CAGGCCTTCACACACAGGGCAGGTGCTTGGCTCAGACCTGCCAAAAGCCATATCCGGG 1229	1230 AGGACCCTGCCCTGACCTAAGCCGACCCCAAAGGCCAAACTGTCCACTCCCTCAGCTCG 1289	1290 GACACCTICICCICCCAGAICCGAGIAACTCCCAAICTICICTGCAGAGGGGAAAT 1349	1350 GTTGTGGAGTGCCCACCGTGCCCAGGTAAGCCAGGCCTGGCCT	1401 CCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCATCCAGGGACAGGCCCCAGCTG 1460	1461 GGTGCTGACGTCCACCTCCATCTCTTCGCACCACCTGCGGCAGCACCGTCA 1517	1518 GTCTTCCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTC 1577	1578	1633 ACGTGGACGGCGTGCATAATGCCAAGACGAAGCCACGGGAGCAGCAGTTCAACA 1692	1693 GCACGTTCCGTGTCACGTCCTCACCGTTGTGCACCAGGACTGGCTGAACGGCAAGG 1752	1753	1813 AAACCAAAGGTGGGACCGGGGGGTATGAGGGCCACATGGACAGAGGCCGGCTCGGCCA 1872	1873 CCCTCTGCCCTGGGAGTGACCGCTGTGCCCAACCTCTGTCCCTACAGGCCACCCCGAGAA 1932	1933 CCACAGGTGTACACCCTGCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCTG 1992
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                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 014643-009040US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 370:
SEQUIBONE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1611.8;
Pred. No. 0;
                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/758,417
FILING DATE: 02-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/21803
FILING DATE: 01-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
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                                                                         WO PCT/US96/16433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 94.3%;
Matches 1722; Conservative
                                                                                                           10-OCT-1996
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                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: W
FILING DATE: 10-OCT-1
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STRANDEDNESS: sing
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US-09-042-353-370
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             2232
2173 TCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCCCCG
                                                                         2205 TCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCG
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Sequence 370, Application US/09042353

Patent No. 6255458

GENERAL INFORMATION:
APPLICANT: Lonberg, Nils

APPLICANT: KAY, KObert M.
TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 421

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,353
FILING DATE: 13-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR DATE: 18-7MX-1992

PRIOR APPLICATION DATA: 1992

PILING DATE: 23-7UN-1992

PRIOR APPLICATION DATA: 05/904,068

PILING DATE: 23-7UN-1992

PRIOR APPLICATION DATA: 07/990,860

FILING DATE: 16-DEC-1992

PRIOR APPLICATION DATA: 08/053,131

PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/096,762

FILING DATE: 26-APR-1993

PRIOR APPLICATION NUMBER: US 08/155,301

FILING DATE: 18-NOV-1993

PRIOR APPLICATION NUMBER: US 08/155,301

FILING DATE: 18-NOV-1993

PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US 08/155,301

FILING DATE: 03-DEC-1993

PRIOR APPLICATION DATA: A
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 18-MAR-1992
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/728 ACT
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10-DEC-1993
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13-MAR-1998
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMDUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: US 08
FILING DATE: 07-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08
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                                                                                                                                                                                                  2265 GGTAATGAGTG 2276
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FILING DATE: 09-MAR
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1922 CCAGGGGCCCCAGCCGGGTGCTCACACCTCCATCTCTTCTCTCTC	RESULT 8 US-07-916-098A-43 US-07-916-098A-43 Sequence 43, Application US/07916098A Septicant: CHISHOLM, PARRICIA L. APPLICANT: THOMAS, DAVID W. SAPPLICANT: ROSA, JOSEPH J. TITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION NUMBER OF SEQUENCES of CORRESPONDENCE ADDRESSE: ADDRESSEE: ALLEGRETTI & WITCOFF, LTD. STREET: 10 SOUTH WACKER DRIVE CITY: CHICAGO
Deet Match 11.74; Score 1611.8; DB 4; Length 4723;	TGCCAAAGCCATATCCGGGAGGACCCTGCCCTGACCTAAGCCGAAGGCCAAAGCCCAAAGCCCAAAGCCCAAAGCCCAAAGCCCAAAGCCCAAAGCCCAAAGCCCAAAGCCCAAAGCCCAAAGCCAAAGCCCAAAGCCCAAAGCCCAAAGCCCAAAGCCCAAAGCCCAAAGCCCAAAGCCCAAAGCCCAAAGCCCAAAGCCCAAAGCCCAAAGCCCAAAGCCCAAAGCCCAAAGCCCAAGCCCAAGCCCAAAGCCCAAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCTCCCAAGCCCAAGCTCCCAAGCTCCCAAGCTCCCAAGCTCCCAAGCTCCCAAGCTCCCAAGCTCCCAAGCTCCAAGCTCCCAAGCTCAAGCCCAAGCTCTCTCT
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                                                                                                                                                    1037
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                        1158 GIGCCCCTACCCCAGGCCCTTCACACACAGGGGCAGGTGCTTGGCTCAGACCTGCCAAAA
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858 GTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAGATCACAAG
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71.6%; Score 1610.8; DB 2; Length 2029;
Best Local Similarity 94.6%; Pred. No. 0;
Matches 1712; Conservative 0; Mismatches 92; Indels 6;
               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/916,098A
FILING DATE: July 24, 1992
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: PCT/US91/08843
FILING DATE: No. 5871732ember 27, 1991
CLASSIFICATION NUMBER: PCT/US91/08843
FILING DATE: No. 5871732ember 27, 1991
CLASSIFICATION NUMBER: O7/618,542
FILING DATE: No. 5871732ember 27, 1990
CLASSIFICATION NUMBER: 26,949
FILING DATE: NO. 5871732ember 27, 1990
CLASSIFICATION NUMBER: 26,949
FELEPRONE; GALS. 115-1000
TELEPRONE: (312) 715-1000
TELEPRONE: (312) 715-1034
TELEPRONE: (312) 715-1234
TELEFAX: (312) 715-1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LOCATION: 1 _... OTHER INFORMATION: /note= "pBAG101 insert" US-07-916-0988-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO PEATURE: NO PEATURE:
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Qy 1935 ACAGGTGTACACCCGCCCCTCCCGGGAGGAGAGAGACCAAGAACCAGGTCAGCCTGACAGAACCAGGTCAGCCTGACAGAGAGAG	TCAGCCTGAC 1994 TCAGCCTGAC 1558	Query Match Best Local Similarity Matches 1587; Conser	70.5%; Score 1584.6; DB 3; Length 2482; ilarity 99.7%; Pred. No. 0; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1995 CTGCCTGGTCAAAGGCTTCTACCCCAGCGACTGCGCGTGGAGTGGGGAGTAGGGCATGGGCCATGGGCCATGGGCCATGGGCCATGGGCCATGGGCCATGGGCAATGGCCAATGAGCCAATGAGCCAATGAGCCAATGAGCCAATGAGCCAATGAGCCAATGAGCCAATGAGCCAATGAGAGAATGAGAGAATGAGAGAATGAGAGAATGAGAGAATGAGAGAATGAGAGAATGAGAGAATGAGAATGAGAATGAGAGAATGAGAGAATGAGAGAATGAGAGAATGAGAGAATGAGAGAATGAGAGAATGAGAGAATGAGAGAATGAGAGAATGAGAGAATGAGAGAATGAGAGAATGAGAATGAGAGAATGAGAATGAGAATGAGAGAATGAGAGAATGAGAATGAGAATGAGAGAATGAGAATGAGAATGAGAATGAATGAGAATGAGAATGAGAATGAGAATGAGAATGAATGAGAATGAGAATGAGAATGAGAATGAATGAGAATGAGAATGAGAATGAATGAGAATGAGAATGAGAAT	GCAATGGGCA 2054	Oy 654 GC Db 688 GC	GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAG 713
Oy 2055 GCGGAGAACAACTACAAGACCACCCCCATGCTGGACTCCGACGGCTCCTTCTTCCT	CCTTCTTCT 2114	Oy 714 AG Db 748 AG	AGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCG 773
Qy 2115 CTACAGCAACGTGACCAAGAGAGCAGGAGCAGGGGAAGGTCTTCTATGCTC	TCTCATGCTC 2174	Oy 774 TG	TGGAACTCAGGGGTCTGACCAGGGGGGGGCACACTTCCCAGCTGTCCTACAGTCCTCA 833
Oy 2175 CGTGATGCATGAGGTTTGCACAACCACTACACGCAGAAGAGCTTTCCCTGTCCCCGGG	IGTCCCGGG 2234	Oy 834 GG	GGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACC 893
Oy 2235 TAAATGAGTG 2244		Oy 894 TA Db 928 TA	TACACCTGCAACGTAGATCACAAGCCCAGCAACGCCAAGGTGGACACTTGGTGAG 953
RESULT 9 US-08-477-460B-3 Conseq 2 hardigation HC/08477460B		Oy 954 AG	AGGCCAGCTCAGGGAGGGAGGGTGTCTGCTGGAAGCCAGGCTCAGCCTCCTGCCTG
Fatent No. 6034223 GENERAL INFORMATION: APPLICANT: Progenics Pharmaceuticals, Inc.		Qy 1014 GC Db 1048 GC	GCACCCCGGCTGTGCAGCCCCAGCCCAGGCAAGCAGGCCGGCC
111LE OF INVENTION: CD4-GAMMA2 AND CD4-19G2 INMUNOCONJUGATES, NUMBER OF SEQUENCES: 9 CORRESPONDENCES. DOCARDO AND CD4-19G2 CONTROL AND CD4-19G2 INMUNOCONJUGATES,	ES, AND USES THEREOF	Qy 1074 CC Db 1108 CC	CGGAGGCCTCTGCCCGCCCCACTCATGCTCAGGAGAGGGTCTTCTGGCTTTTTCCACC 1133
STREET: 30 Rockefeller Plaza CITY: New York STATE: New York		Oy 1134 AG Db 1168 AG	AGGCTCCAGGCAGGCACGCTGCCCCTACCCCAGGCCCTTCACACACA
ZIP: 10112 ; COMPUTER READABLE FORM: ; MEDIUM TYPE: Floppy disk		Oy 1194 GT 	GIGCITGGCTCAGACCTGCCAAAAGCCATATCCGGAAGACCCTGCCCCTGACCTAAGCC 1253
COPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.24 CURRENT APPLICATION DATA:		Qy 1254 GA - Db 1288 GA	GACCCCAAAGGCCAAACTGTCCACTCCCTCAGCTCGGACACCTTCTCTCCTCCCCAGATCC 1313
AFFICATION NUMBER: US/08/47/,460B FILING DATE: 07-41N-1995 CLASSIFICATION: 530 FRIOR APPLICATION DATA:		Oy 1314 GA Db 1348 GA	GAGTAACTCCCAATCTTCTCTCTGCAGAGCGAAATGTTGTGTCGAGTGCCCACCGTGCC 1373
AFFICATION NOMBER: 05 0/92/,931 ; FILING DATE: 07-4UG-1992 ; ATTORNEY/AGENT INFORMATION: ; NAME: White, John P. ; BEGIGHDARD WIMPER: 0,000 P.		Qy 1374 CA Db 1408 CA	CAGGTAAGCCAGCCCAGGCCTCGCCCTCCAGCTCAAGGCGGACAGGTGCCCTAGAGTAG 1433
TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 977-9560		Qy 1434 CC Db 1468 CC	CTGCATCCAGGACAGGCCCCCAGCTGGTGCTGACACGTCCACCTCCATCTTCCTCA 1493
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:		Qy 1494 GC Db 1528 GC	GCACCACCTGCGGCAGCACCGTCAGTCTTCCTCTTCCCCCCAAACCCCAGGACACCCTC 1553
TENSIN: 275. Dase pails TENSIN: TOTOLOGY: unknown MATEGILE TOTOLOGY: unknown MATEGILE TOTOLOGY:	•	Qy 1554 AT Db 1588 AT	ATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGACGTGAGCCACGAAGACCCC 1613
ORIGINAL SOURCE: ORGANISM: home sapien CELL TYPE: lymphocyte		Qy 1614 GA Db 1648 GA	GAGGICCAGITCAACTGGIAACGIGGACGGCGTGGAGGTGCATAATGCCAAGACAAGCCA 1673
0,900,000,000,000,000,000,000,000,000,0		Qy 1674 CG	CGGGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAG 1733

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<u>ئ</u> ۾	1734 GACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCC 1793 	65 G	774 TGGAACTCAGGCGCTCTGACCAGCGCGCGCACACCTTCCCAGCTGTCCTACAGTCCTCA 833
දුරු සි	1794 ATCGAGAAAACCATCTCCAAAACCAAAGGTGGGACCCGCGGGGTATGAGGGCCACATGGA 1853 	% d	834 GGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACC 893
SP GS	1854 CAGAGGCCGCCTCGGCCCTCTGCCCTGGGAGTGACCGCTGTGCCAACTTCTGTCC 1913	\$ Q	894 TACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAGGTGGACAACAGTTGGTGGG 953
SP GS	1914 TACAGGGCAGCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGAGGAGATGAC 1973	& 8	954 AGGCCAGCTCAGGGAGGGAGGGTCTGCTGGAAGCCAGGCTCAGCCTCCTGCCTG
cy do	1974 CAAGAACCAGGTCAGCCTGACCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGT 2033 	S S	1014 GCACCCCGGCTGTGCAGCCCCAGCCCAGGGCAGGAGGCCCCCATCTGTCTCCTCAC 1073
Qy Dp	2034 GGAGTIGGGAATGGGCAGCGGGAGAACAACTACAAGACCACACCTCCCATGCTGGA 2093 	y d	1074 CCGGAGGCCTCTGCCCGCCCCACTCATGCTCAGGGAGGGTCTTCTGGCTTTTTCCACC 1133
Pp Oç	2094 CTCCGACGGCTCCTTCTTCTTCTACAGCAAGCTCACCGTGGACAAGACAGGTGGCAGCA 2153 2128 CTCCGACGGCTCCTTCTTCTTCTTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGGA 2187	y d	1134 AGGCTCCAGGCAGGCACAGGCTGGGTGCCCTACCCCAGGCCCTTCACACACA
Oy Dp	2154 GGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACACCACTACACGCAGAA 2213	& dd	1194 GIGCITGGCTCAGACCTGCCAAAAGCCATATCCGGGAGGACCCTGCCCCTGACCTAAGCC 1253
oy Dp	2214 GAGCCTCTCCCTGTCCCCGGGTAAATGAGTG 2244	% q	1254 GACCCCAAAGGCCAAACTGTCCACTCCCTCAGCTCGGACACCTTCTCCTCCCTC
RESULT US-08-3	RESULT 10 US-08-379-516-3	oy dd	1314 GAGTAACTCCCAATCTTCTCTCTGCAGAGGCAAATGTTGTGTCGAGTGCCCACCGTGCC 1373
	sequence 5, Application US/U83/9516 Setent NO. 6083478 GENERAL INFORMATION: APPLICANT: Allaway, Graham P.	o d	1374 CAGGTAAGCCAGCCCAGGCCTCCAGCTCCAAGGCGGGACAGGTGCCCTAGAGTAG 1433
	LICANT: Maddon, Paul J. LICANT: Maddon, Paul J. E. OF INVENTION: No. 6083478-Peptidyl Moiety-Conjugated CD4-Gamma2 and CD4-IgG2 E. OF INVENTION: Immunoconjugates and Uses Thereof E. REFERENCE: 4125-A-PCT-US	S d	1434 CCTGCATCCAGGACAGGCCCCAGCTGGGTGCTGACAGGTCCACCTCCATCTCTTCTCA 1493
COKK CURRI EARL EARL	CURKENT PELLINON NOWBER: US/08/3/9,016 CURRENT FILING DATE: 1996-06-10 EARLIER APPLICATION NUMBER: PCT/US93/07422 EARLIER PILING DATE: 1993-08-06 PARLIER PADITON NUMBER: PCT/US93/07422	ò a	1494 GCACCACCTGCGGCAGCACCGTCAGTCTTCCCCCCCAAAACCCAAGGACACCCTC 1553
	EARLIER FILING DATE: 1992-08-07 NUMBER OF SEQ ID NOS: 9 FORTHARE: Patentin Ver. 2.1	ò q	1554 ATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGACGTGAGCCACGAGAACACCCC 1613
LEN LEN TYP ORG	TYPE: DNA TYPE: DNA TYPE: DNA TSOGANISM: Homo sapiens	ò qa	1614 GAGGTCCAGTTCAACTGGTACGTGGACGCGTGGAGGTGCATAATGCCAAGACAAAGCCA 1673
Query Best Match	Query Match Query Match Dest. 6; DB 3; Length 2482; Best Local Similarity 99.7%; Pred, No. 0; Marches 1587. Concernative 0. Mismatches	\$ &	1674 CGGGAGGAGCAGTTCAACAGCACGTTCCCGTGAGCGTCCTCACCGTTGTGCACCAG 1733
à	AAGGGCCCATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAG 71	, yo da	1734 GACTGGCTGAACGCCAAGGAGTACAAGTGCAAGGTCTCCAACAAGGCCTCCCAGCCCCC 1793
a &	688 GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAG 747 714 AGCACAGCGGCCCTGGGCTGCTCAAGGACTACTTCCCCGAACCGGTGAGGGTGTCG 773	λö	1794 ATCGAGAAAACCATCTCCAAAACCAAAGGTGGGACCCGCGGGGGTATGAGGGCCACATGGA 1853

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Sat Jul 19 10:01:51 2003 sat Garden Garde	RESULT 1915-91-91-91-91-91-91-91-91-91-91-91-91-91-

1314 GAGTAACTCCCAATCTTCTCTGCAGAGCGCAAATGTTGTGTCGAGTGCCCACCGTGCC 1373

ADDRESSEE: Cooper & Dunham STREET: 30 Rockefeller Plaza CITY: New York STATE: New York COUNTRY: USA ZIP: 10112 COMPUTER READABLE FORM: MEDIUM TYPE: RIOPPY disk COMPUTER: IBM PC Compatible COMPUTER: IBM PC Compatible COMPUTER: DEAD FOLDOS/MS-DOS SOFTWARE: PatentIn Release #1.24 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/409,006A	-SEP-1999 424 424 A24 A24 A124 A129 ANTA: US 07/927,93 BRT: US 08 BRS: US 678 BRS: US 678 BRS: US 08 US 077-9809 OOP UI USTICS: SE pairs Cid Wn NA	Query Match 70.5%; Score 1584.6; DB 4; Length 2482; Best Local Similarity 99.7%; Pred. No. 0; Matches 1587; Conservative 0; Mismatches 4; Indels 0; Gaps 0; Qy 654 GCCCCACAGGGCCCATCGCTCTCCCCTGGCCCTGGTCCAGGAGCACCTCCGAG 713 Pin	0
1378 GAGTAACTCCCAATCTTCTCTGCAGAGCGCAAATGTTGTGTCGAGTGCCCACCGTGCC 1407 1374 CAGGTAAGCCAGCCCTGCCCTCCACCTCAAGGCGGCACAGGTGCCCTAGAGTAG 1438 1408 CAGGTAAGCCCAGGCCTCGCCTCCAGCTCAAGGCGCGCTAGAGTAG 1467 1434 CCTGCATCCAGGCACAGGCCCTCGAGCTCACCTCCATCTTCCTCA 1493 1468 CCTGCATCCAGGACAGGCCCCAGCTGGTGCTGACACCTCCATCTTCCTCA 1493 1468 CCTGCATCCAGGACAGGCCCCAGTGGTGCTGACACCTCCACCTTCCTCTC 1527 1468 CCTGCATCCAGGACACGCTCAGTTCTCTCTCTTCCTCTCTTCTTCTTCTTCTTCTTCTTCT	ATGATCTCCCGGACCCCTGAGGTCACGTGGTGGTGGACGTGAGCCCCCTGAGGACCCCCTGAGGACCCCCTGAGGACCCCCTGAGGACCCCCTGAGGACCCCCTGAGGACCCCCTGAGGACCCCCTGAGGACCCCCTGAGGACCCCCTGAGGACCCCCTGAGGACCCCCTGAGGACCCCCTGAGGACCCCTGAGGACCCCAGGAGACCCCTGTGGAGCCTGGAGCCTGAGGAGCCAGAGCCAGAGCCAGTTCAACTGGTAACTGGTAGGAGCGTGGAGGAGTGCATAATGCCAAGACAAAACCCAGTACATGGTAACTGGTAACTGGAAGACGACGTTGTGCATAATGCCAAGACAAAACCCAGTTCAACAGAGCCAGTTCAACAGAGCCAGGAGGAGAGCAGAGCCAGAGCCAGAGAGAGAGAGAGAGAGAGAGAAAACCATCAACAGAACACACAGCAGAGCACGTTGTGAACAGAAAACCCTCAACAGAAAACCCTCCAAGAAAACCCAAAAAAAA	Qy 1914 TACAGGGCAGCCCGAGAACCACAGGTGTACACCCTGCCCCATCCCGGGAGATGAC 1973 Db 1948 TACAGGGCAGCCCGAGAACCAGCTGCCCCTCCCGGGAGGAGATGAC 2007 CA 1974 CAAGAACCAGGTCACCTGCTCAACAGCTTCTACCCCGGGAGATGAC 2007 CA 1974 CAAGAACCAGGTCACCTGGTCAAAGGCTTCTACCCCGGCGACATGCCGT 2033 CA 1974 CAAGAACCAGGTCAGCTGGTCAAAGGCTTCTACCCCAGCGCATCGCCGT 2033 CA 2034 GAAGAGGAACAGCTGACTGCTGGTCAAAGGCTTCTACCCCAAGCGCATCGCCGT 2067 Qy 2034 GAAGTGGAAACAGCAACCAACACACACCACCTCCCATGCTGGA 2127 Qy 2094 CTCCGACGGCTAATGGAGAACCAACCAACACACACCTCCCATGCTGGA 2153 Db 2128 CTCCGACGGCTCCTTCTTCCTTACAGCAAGCTCACCGTGGACAAGGTGGCAGCA 2187 Qy 2124 GGGGAACGCTCCTTCTTCTTCTTCTTCAAGCATCACCGTGGACAAGGGTGGCAGAA 2213 Db 2128 CTCCGACGGCTCCTTCTTCTTCTTCTTCTTCTTCTTCTCTGAAGCTCACCTGCACAACACACCACACACA	Oy 2214 GAGCCTCTCCCTGTCCCCGGGTAAATGAGTG 2244 Db 2248 GAGCCTCTCCCTGTCTCCGGGTAAATGAGTG 2278 RESULT 13 US-09-409-006A-3 Sequence 3, Application US/09409006A Patent No. 6342586 APPLICANT: Progenics Pharmaceuticals, Inc. TITLE OF INVENTION: TITLE OF SEQUENCES: CORRESPONDENCE ADDRESS:

OY 2214 GAGCCTCTCCCGGGGTAAATGAGTG 2244 Db 2248 GAGCCTCTCCCTGTTCCCGGGTAAATGAGTG 2278	0/Sn 1	bedudry, Cary A. Maddon, Paul J. VENTION: CD4-GAMM. BEQUENCES: 9 SINCE ADDRESS: COODER & Dunham	STREET: 1185 Avenue of the Americas CITY: New York STATE: New York COUNTRY: ISA	036 EAL YPE	SYSTEM: PC COMPACIDI SYSTEM: PC-DOS/N PATENTIN Release LICATION DATA:	FILING DATE: 07-UN-1995 CLASSIFICATION: 435 ATTORNEY/AGANT INCRMATION: NAME: White		TELEFANE: (212) 2/8-0400 TELEFAN: (212) 391-0525 TELEFX: T	LENGTH: 2482 base pairs TYPE: nucleic acid TRANDEDESS: double TOPDIAGY. unbown	2.0.6	70.5%;					
Oy 1134 AGGCTCCAGGCAGGCACGGCTGGGTGCCCTACCCCAGGCCCTTCACACAGGGGAG 1193 Db	09 1194 GTGCTTGGCTCAGACCTGCCAAAAGCCATATCCGGGAGGACCCTGCCCCTGACCTAAGCC 1253	1314 GAGTAACTCCCAATCTTCTCTCTCAGCTCGGACACCTTCTCTCTC	1374 CAGGTAAGCCAGCCCAGGCCTCCAGCTCAAGGGGGGACAGGTGCCCTAGAGTAG 1433 	1434 CCTGCATCCAGGACAGGCCCCAGCTGGGTGCTGACACGTCCACCTCCATCTCTCTC	1494 GCACCACCTGCGGCAGCACCGTCAGTCTTCCCCCCCAAAACCCAAGGACACCCTC 1553 	1554 ATGATCTCCGGACCCCTGAGGTCACGTGCGTGGACGTGGACGTGAGCCACGAAGACCCC 1613 	1614 GAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAGCCA 1673 	1674 CGGGAGGAGCAGTICAACAGCACGTICCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAG 1733 1708 CGGGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCACCGTTGTGCACCAG 1767	1734 GACTOGCTGAACGGCAAGGAGTACAAGTGCAAGAAAAGGCCTCCCAGCCCCC 1793 	1794 ATCGAGAAAACCATCTCCAAAACCAAAGGTGGGACCCGGGGGGTATGAGGGCCACATGGA 1853 	1854 CAGAGGCCGGCTCGACCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCC 1913	1914 TACAGGGCAGCCCCGAGAACCAGGTGTACACCCTGCCCCATCCCGGGAGGAGAGAGA	1974 CAAGAACCAGGTCAGCCTGACCTGCTGGTCAAAGGCTTCTACCCCAGGACATCGCCGT 2033 2008 CAAGAACCAGGTCAGCCTGACCTGCTTCTACCCCAGGACATCGCCGT 2033	4 GGAGTGGGAGGCAATGGCTGAGAAACAATACCAGCGACATCGCGT 5 GGAGTGGGAGCAAGCGAGGAAACAACAACAACAACACACAC	2094 CTCCGACGCTCCTTCTTCCTCTACAGCAACCTCACGAGCAAGCA	2154 GGGGAACGTCTTCTCATGCTCCGTGATGATGCATGCACACACA

1828 1854 1914 1974 1974	GRAGIGGGAGGGAGCAGCCGGAGAACTACAAGACCACCCCCCATGCTGGAGGGAG	Search completed: July 18, 2003, 19:59:05 Job time : 124.256 secs			
	954 AGGCCAGCTCAGGAGGAGGGTGTCTGCTGGAGGCCAGGCTCCTGCCTG	GTGCTTGGCTCAGACCTGCCAAAAGCCATATCCGGGAAGACCCTGCCCCTGACCTAAGCC GTGCTTGGCTCAGACCTGCCAAAAGCCATATCCGGGAAGACCCTGCCCCTGACCTAAGCC GTGCTTGGCTCAGACCTGCCAAAAGCCATATCCGGAAGACCCTGCCCCTGACCTAAGCC GACCCCCAAAGGCCAAACTGTCCACTCCCTCAGGTCGGACCTTCTCTCTC	CAGGTAAGCCAGCCCTGCCCTCCAGCTCAAGGCGGGACAGTGCCCTAGAGTAGCAGTAGCAGCCCTAGAGTAGCAGTAGCAGTAGCCCTAGAGTAGCAGTAGCAGTAGCAGCCCTAGAGTAGCAGGTAAGCAGGCAG	1554 ATGATCTCCCGGACCCCTGAGGTCACGTGGTGGTGGTGGTGGTGGCACGAAGACCCC 1613	1734 GACTGGCTGAAGGGGTACAAGTGCAAGGTCTCCAACAAGGCCTCCCAGCCCCC 1793 1768 GACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCC 1827 1794 ATCGAGAAAACCATCCCAAAACCAAAGGTGGGCCCCGGGGGTATGAGGCCTCCAGGGCTTCTCAAAAGTGTGTGGAAAGTGTGGAAAGTGTGGAAAGTGTGGAAAGTGTGGAAAGTGTGGAAAGTGTGTGTGTGTGTGAAAAGTGTGAAAAGTGAAAAGTGGAAAGTGTGTGTTTTTT

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AF103772 Homo Sapi AF193852 Homo Sapi X63398 H. Sapiens D AP001238 Homo Sapi AC110080 Homo Sapi AC110389 Homo Sapi AF103536 Homo Sapi AF103486 Homo Sapi AF103489 Homo Sapi AF034164 Homo Sapi AF043164 Homo Sapi AF043164 Homo Sapi AF043164 Homo Sapi AF043164 Homo Sapi AF103771 Homo Sapi PRI 17-FEB-1993 U86803 Human Ig ka X72462 H.sapiens m AX258845 Sequence L03152 Homo sapien AY043092 Homo sapi AY043138 Homo sapi U97250 Homo sapien L26890 Homo sapien L08900 Homo sapien AX258847 Sequence AX258851 Sequence AX258895 Sequence L03156 Homo sapien AB063945 Homo sapi AY043160 Homo sapi AF035044 Homo sapi AX258847 Sequence X72440 H.sapiens m AR162137 Sequence L09083 Homo sapien AY043139 Homo sapi 200004 Human germl M23848 Human Ig re Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 327) L01279 Homo sapien AF107244 Homo sapi AJ010446 Homo sapi AF146408 Homo sapi AY043133 Homo sapi X70450.1 GI:38436 anti-DNA antibody; complementarity determining region; Ig kappa light chain; Ig light chain; Ig variable region; IgM; immunoglobulin; systemic lupus erythematosus. score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. אסס מאבאורייייי 327 bp DNA linear PRI I H.sapiens DNA for anti-DNA antibody light chain variable region, subgroup V(K) I (III-2R IgM line). X70459 ALIGNMENTS SUMMARIES AY043138 HSU97250 HUMIGKVJAA HUMFRAQ HSIGKLV41 AX258845 AX258851 AX258895 HUMIGHGU HSIGKLV55 HSIGKLV25 HSIGKLV19 AF107244 HSA010446 AY043139 HSIGK6 HSIGKVBAC AF099196 AY043164 HUMIGHGO HSIGDPK4 AY043092 AF146408 AY043133 HUMIGKAH AF103772 AF193852 HUMFRBH Query Match Length Homo sapiens. Homo sapiens REFERENCE

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
(and 138)
Pritsch,O., Magnac,C., Dumas,G., Egile,C. and Dighiero,G.
V gene usage by seven hybrids derived from CD5+ B-cell chronic
lymphocytic leukemia and displaying autoantibody activity
eloci 82 (10), 3109-3112 (1993)
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Pritech, O., Magnac,C., Dumas,G., Egile,C. and Dighiero,G.
Direct Submission
Submitted (24.JAN-1997) Unite d'Immunohematologie et
d'Immunopathologie, Institut Pasteur, 28, rue du Dr. Roux, Paris
75724, France
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Human Ig kappa chain V-region (VL-COL) mRNA, partial cds.
U86803.1 GI:1864136
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Manheimer-Lory, A., Katz, J.B., Pillinger, M., Ghossein, C., Smith, A. and Diamond, B.
Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype J. Exp. Med. 174 (6), 1639-1652 (1991) 92078875
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Insulin and igf-1 receptor agonists and antagonists
Patent: WQ 0172771-A 2352 04-0CT-2001,
DGI, BioTechnologies, L. L. C. (US); Novo Nordisk A/S (DK)
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//note="complementarity determining region, CDR 2"
265. 285
/note="complementarity determining region, CDR 3"
a 89 c 77 g 77 t
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llarity 100.0%; Pred. No. 1.8e-94;
Conservative 0; Mismatches 0; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="IgM light chain variable region"
71. .102
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Sequence 2352 from Patent WO0172771.
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AX258853.1 GT:16508406
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/trānslation="MRVPAQLLGLLLMLPDTKCDIOMTQSPSSLSASVGNRVTITCR
ASQGISNYLAWYQQKPGKVPKLLIYAASTLQSGVPSRFSGSGSGTDFSLTISSLQPED
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                                                                                                                                    /clone="I.40"
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/db_xref="GI:441193"

    .395
/product="Ig kappa light chain (VJC)"

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Pred. No. 7.1e-86;
0; Mismatches 6
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Sequence 2344 from Patent WO0172771.
AX258845.
AX258845.1 GI:16508398
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                                                                    /organism="Homo sapiens"
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chromosome="2"
                                Location/Qualifiers
1. .395
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346. .384
/note="J-Kappa 1"
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97.28;
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Matches 317; Conserv
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                                                                                                                                                                                                                       /product="Ig kappa chain V-region"
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KVEIKKRRARA"
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H.sapiens mRNA for rearranged Ig kappa light chain variable region
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Klein,R., Jaenichen,R. and Zachau,H.G.
Expressed human immunoglobulin kappa genes and their hypermutation
Eur. J. Immunol. 23 (12), 3248-3262 (1993)
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Submitted (26-APR-1993) H.G. Zachau, Institut fuer Physiologische
Chemie, der Universitaet Muenchen, Schillerstr 44, 8000 Muenchen;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 395)

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X72462.1 GI:441392
C-region; immunoglobulin; J-segment; kappa light chain; V-region.
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                                                                /map="2p11-p12"
/cell_type="B cells"
/note="patient with chronic lymphocytic leukemia"
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Pred. No. 7.2e-86;
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              /organism="Homo sapiens'
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                                                                                                                                                                 /gene="VL-COL"
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Matches 317; Conservative
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AB063945
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/product=1immunoglobulin gamma-chain, V region"
/protein_id="AAA52924.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68 GCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  128 TICCTAAGCICCIGAICTAIGCIGCAICCACTITGCAAICAGGGGICCCAICTCGGITCA 187
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens
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98.1%; Pred. No. 3.6e-85;
tive 0; Mismatches 3;
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/dev_stage="bone marrow"
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/tissue_lib="BWHIV"
<1.547
/gene="iGHV@"
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/gene="IGHV@"
/note="G00-128-528"
1 119 c 108 g
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/gene="IGHV@"
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Best Local Similarity 98.1;
Matches 313; Conservative
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// Ante="unmaned protein product |
// Antenslide"(Able=11 |
// Able=11 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
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A binary plasmid system for shuffling combinatorial antibody libraries Proc. Natl. Acad. Sci. U.S.A. 89 (21), 10026-10030 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 ATCACTTGCCGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
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            Patent: WO 0172771-A 2344 04-0CT-2001;
DGI BioTechnologies, L.L.C. (US) ; Novo Nordisk A/S (DK)
Location/Qualifiers
1. 761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 91.3%; Score 298.4; DB 6; Length 761; Best Local Similarity 97.2%; Pred. No. 3.1e-85; Matches 315; Conservative 0; Mismatches 6; Indels 3;
                                                                                                                                                      /organism="synthetic construct'/db_xref="teaxon:32630"
//note="synthetic DNA"
/100te="synthetic DNA"

    .447
    /organism="Homo sapiens"

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L03152.1 GI:185387
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HUMIGHGQ
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g ò qq ò g ð Db ò g ò

7

Gaps

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<1. . > 328
/codon start=1
/codon start=1
/product="immunoglobulin light chain variable region"
/protein_id="AAK94864.1"
/protein_id="AAK94864.1"
/db xxef="d:18025710"
/translation="IQMTOgPSSLGASUGDRVTITCRASQGISNYLAWYQQKPGKVP
KLLIYAASTLQSGVPSRFSGGSGGTDFTLTISSLQPEDVATYYCQKYNSAPRMYTFGQ
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Homo sapiens clone FD2K myosin-reactive immunoglobulin light chain variable region mRNA, partial cds.
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             Ghiotto, F., Fais, F., Valetto, A., Albesiano, E., Allen, S., Schlman, P., Vinciguerra, V., Rai, K., Ferratini, M. and Chiorazzi, N. Ig VL gene repertoire in B cell type chronic lymphocytic leukemia Unpublished
                                                                                            2 (bases I to 328)
And Motto, F., Rais, F., Valetto, A., Albesiano, E., Allen, S.,
Schulman, P., Vinciguerra, V., Rai, K., Ferrarini, M. and Chiorazzi, N.
Direct Submission
Submitted (29-d707-2001) North Shore-LIJ Research Institute, 350
Community Drive, Manhasset, NY 11030, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAAACAGTGCCCCTCGTATGTACACTTTT 300
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                                                                                                                                                                                                                                                                                                   /db xref="taxon:9606"
/ceIl type="B lymphocyte from patient with IgM+ chronic
lymphocytic leukemia (CLL)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GACATCCAGATGACCCAGTCTCCATCCTCCTGTCTGCATCTGTAGGAGACAGAGTCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 296; DB 9; Length 328;
Pred. No. 1.9e-84;
0; Mismatches 10; Indels
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/isolate="MCLL141"
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06
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Best Local Similarity 96.0
Matches 315; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="immunoglobulin kappa light chain VLJ region"
/protein id="BAC01573.1"
/b_xref="GI:2166907"
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KLLIYAASTLQSGVPSRFSGSGGTDFTLTISSLQPEDVATYYCQKYNSAPRTFGGGT
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Homo sapiens MCLL141 immunoglobulin light chain variable region
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

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XS Kurosawa,Y.

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Comprehensive Medical Science, Fujita Health University;

Kutsukske-cho, Toyoake 470-1192, Japan

(E-mail:kurosawa@tijita-hu.ac.jp, Tel:81-562-93-9387)

Please visit our web site

URL:http://www.fujita-hu.ac.jp/immunity/.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                       /clone_lib="AIMS4"
/note="mixture of tissues:tonsils, umbilical cords,
peripheral blood and bone marrow"
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Pred. No. 7.8e-85;
0; Mismatches 8;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="K118"
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/gene="IGK"
/codon_start=1
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Best Local Similarity 96.6%;
Matches 315; Conservative
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us-09-627-896b-25.rge	FEATURES DGI Biorechnologies, L.L.C. (US); Novo Nordisk A/S (DK) CDS //Caganism="synthetic construct" CDS //Caganism="synthetic construct" And xarefield A thetic DA," COGO = "YAH thetic DA,"	Chockern id="CAD10172." Chockern id="CAD10172." Chockern id=08401." EMPWGRIKSKUDGGTPUYLBSGGGLWEGGSERLSCAASGFTFSNAWWSWVROAPGKGTPUYLBSGGGGGSGGGGGSGGGGSGGTFSNAWWSWVROAPGKGGTPUYLBSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	90 %	0y 181 CGGTTCAGTGGATCTAGTTAGTGATCAGTGGATCGATCAGGGGGTCCCATCT Db 604 CGGTTCAGTGGATCTGGGAAAATCAGTTGCAATCAGGGGTCCCATCT 180 Oy 241 GAAGATGTGGAACTGGGAAAAGATTCACTCTCACCATCAGGGGTCCCATCT 603 Db 664 GAAGATGTGGAACTTATTACTGCAGATTTCACTCTCAGCAGCTGCAGCTTC 603 Oy 301 GAAGATGTGGAACTTATTACTGCAGATTTCACTCTCAGCAGCTTCAGCAGCTT 603 Oy 301 GAAGATGTAGGAACTTATTACTGCAAAAGTATAAAGTATAACAGTCCCCTCCGAGCCT 663 Db 721 CTGGGAACTTATTACTGTCAAAAGTATAAAGTATCACATCCCGATACGTTCGGC 300 721 CTGGGAACTAGAAATCAAA 324	PAT 26-OCT-2		
nol. Immunopathol. 87 (2), 184-192 (1998)	Direct Submit Nedicii Houstoir	/ / / / / / / / / / / / / / / / / / /	1 GACATCCAGATGACCAGCTCATCCATCCTCCATCTCTGATGATGATGATCACCAGTCTCCATCCTCTGTGTGTG	A THE STEE STEE	RESULT 10	Basiey,J., Basiey,J., Brisserte,R., Insulin and Patent: WO O	

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Homo sapiens cell-type T-cell immunoglobulin gamma-chain, V région
(GHVW) mRNA, partial cds.
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LIYAASTLQPGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCQKYNSAPRTFGQGTKV
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 450)
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A binary plasmid system for shuffling combinatorial antibody libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAAACAGTGCCCCT----TTCACTTTCGGC
                                                                                                                                                                             GACATCCAGATGACCCAGTCTCCATCCTCCTGTCTGCATCTGTAGGAGACAGAGTCACC
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                                                                         Length 761;
                                                                                                           Indels
                                                                     Score 295.2; DB 6;
Pred. No. 3.3e-84;
0; Mismatches 8;
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ATYYCQKXNSAPYTFGGGTKLEIK"
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Mandecki,W.S.,
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                                                                                                                                                                                                              Length 752;
                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                DB 6;
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Cocganiam="synthetic construct"
(db_xref="taxon:32630"
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                                                                                                                                                                                                            Query Match 90.3%; Score 295.2; DB 6 Best Local Similarity 96.6%; Pred. No. 3.3e-84; Matches 313; Conservative 0; Mismatches 8
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Choi.1.4., Park.S.G., Chung,J.H., Kim,I.J. and Hong,H.J.
Direct Submission
Submitted (12-007-1999) Microbiology, College of Medicine, INJE
University, 633-165 Gaegum-Dong Jin-GU, Pusan 614-735, South Korea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <1. .>316
/note="Fab monoclonal antibody against preSl of hepatitis
                                                                                                                                                                                                                                                                               61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 GAAGATGTTGCGACTTATTACTGTCAAAAGTATGACAGTGCCCCTC---GCACTTTCGGC
                                                                                                                                                                                                        1 GACATCCAGATGACCCAGTCTCCATCCTCCTGTTGCATCTGTAGGAGACAGAGTCACC
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                                                                                                                                                                      Gaps
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                                                                                                                              Query Match

88.4%; Score 289.2; DB 9; Length 390;
Best Local Similarity 95.1%; Pred. No. 3e-82;
Matches 310; Conservative 0; Mismatches 13; Indels 3;
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1 (bases 1 to 390)
Chukwuocha, R. U., Hfiao, E., Shaw, P., Witztum, J. L. and Chen, P. P.

Isolation, characterization and sequence analysis of five IgG monoclonal anti-phospholipid Fab fragments generated by phage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  242 TIGCAACTIAITACIGICAAAAGIAIAACAGIGCCCCIC---GGACGIICGGCCAAGGGA
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                                                                                                                                                                      Gaps
    EIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPERPKYSGRWIT"
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                                                                                                                                  Score 290.2; DB 9; Length 450;
Pred. No. 1.4e-82;
0; Mismatches 8; Indels 3
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a 120 c 110 g
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                                                                                                                           88.7%; initianity 96.6%; Interpretation 0;
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AF103772
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KLLIYAASTLQSGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCQKYNSAPLGGGTKV
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                                                                                       Query Match 88.4%; Score 289; DB 9; Length 316; Best Local Similarity 95.7%; Pred. No. 3.5e-82; Matches 311; Conservative 0; Mismatches 5; Indels
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UI-HF-BLO UI-HF-BLO 602712592 AV733746 AGENCOURT UI-HF-BLO

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BG684416 826 bp mRNA linear EST 01-MAY-2001
602636169F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4763993 5',
mRNA sequence.
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BG756818 602710291
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BG756188 6
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BG756818
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BG684027
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BG341944 602463276
BG341941 602463283
BQ8B1840 AGENCOURT
BM509065 ihi6b08.x
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                                                                                                                                            July 18, 2003, 04:16:54; Search time 566.66 Seconds .(without alignments) 9345.860 Million cell updates/sec
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Copyright (c) 1993
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AGENCOURT 602498773 AGENCOURT UI-HF-BLO UI-HF-BLO

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

(Dases 1 to 959)

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60246328381 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4576124 5',
mRNA sequence.
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BG341941.1 GI:13148379
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/tissue type="primary B-cells from tonsils (cell line)"
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B. (Dases I to 957)

S. NIH-MGC http://mgc.nci.nih.gov/

L. Unpublished (1999)

Contact: Robert Strauberg, Ph.D.

Email: Gapbs-remail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Arrayed by: The I.M. A.G. E. Consortium (LINL)

Conda Library Arrayed by: The Condendation and the Condendation and through the I.M.A.G.E. Consortium (LINL)

Clone distribution: MGC clone distribution information can be thusp://image.llm.gov

Plate: LLCMI288 row: g column: 19
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BG341934.1 GI:13148372
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Best Local Similarity 97.5%; Pred. No. 1.6e-86;
Matches 318; Conservative 0; Mismatches 5; Indels 3; Gaps
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                                                                                                                                                  /clone lib="NIH MGC L8"
/clone lib="NIH MGC L8"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab host="bland"y B-cells from tonsils (cell line)"
/lab host="bland"y B-cells y Vector: poTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G): Size-selected >500pf for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II T (Life Technologies).
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BQ881840 888 bp mRNA linear EST 16-AUG-2002
AGENCOURT_8642888 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6295725
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

I (bases I to 888)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        234 CGGTTCAGTGGCAGTGGCTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GACATCCAGATGACCCAGTCTCCATCCTCCTGTTCTGCATCTGTAGGAGACAGAGTCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             174 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT
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                                                                                                                                                                                                                                                                                                                                                                                                                             Score 302; DB 12; Length 959;
Pred. No. 1.8e-86;
0; Mismatches 5; Indels
found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLCM1288 row: e column: 21
High quality sequence stop: 616.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
                                                                                                        organism="Homo sapiens"
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                                                                                                                           /db_xref="taxon:9606"
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BQ881840
BQ881840.1 GI:22273848
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Best Local Similarity 97.5%;
Matches 318; Conservative
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/lab host="DH10B (phage-resistant) priming. Directionally cloned
/lab host="DH10B (phage-resistant)"
/lab host="DH10B (phag
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 626)
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BMS09065
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate:.LLCMS502 row; g column: 22
High quality sequence stop: 655.
Location/Qualifiers
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Home sapiens

Bukaryota; Merazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Bukaryota; Merazoa; Chordata; Catarrhini; Hominidae; Homo.

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 358)

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Pr. D.

Email: Capaba: Town at the beginning of the sequence.

Contact: Robert Strausberg, Pr. D.

Eco RI site shown at the beginning of the sequence.

CDNA Library Preparation: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be town through the I.M.A.G.E. Consortium/LLNL at:

Location/Darpy/mage/image/image.html

Seq primer: M13 Forward.

Ab_zref="taxon:966" (clone information can be www-bio.lln.gov/bbrp/image/image.html

Location/Oblapy/mage/image.html

Location/Darpy Maria Center B cells"

Ab_zref="taxon:966" (clone="ib=NHH MGC 37" (clone="ib=NHH MGC 37" (clone="ib=NHH MGC 37" (clone="ib=NHH MGC 37" (clone="ib=NHH MG 27" (clone="ib=NHH MG Coll type="ig=mimuted" from size fractionaled graph aria de Fatima (constructed from size fractionaled" (clone="vector: pr773-ac; site_1: Not!; site_2: sbo NI; clone="vector: pr773-ac; site_1: Not!; site_2: sbo NI; clone="vect
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935 bp 'mRNA linear EST 27-FEB-2001

62463029F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4575847 5',

RG342083.1 GI:13148509
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Pred. No. 5e-79;
0; Mismatches 8; Indels 0;
                              IMAGE:3057865 5', mRNA
                                                    AW404145
AW404145.1 GI:6923202
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Local Similarity 97.3%;
es 283; Conservative (
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/db xerf="texon.9606"
/clone lib="Human insulinoma"
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/lab=bost="blane"
/lab=bost="blane"
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Xhol; Site 2: EcoRI; Constructed with lambda ZAPII system
(Stratagene) by Dr. H. Inoue following the Washington
University protocol
(http://genome.wustl.edu/est/lambda_protocol.shtml)
Please contact Hiroshi Inoue, MD/PhD for further
information on this library (Metabolism Divisaion, Permutt
Laboratory, Washington University School of Medicine, Box
8127, 6605 Euclid Ave, St. Louis, MO 63110). Note: this
is a Washington University Pancreas EST project library. "
AL Dackson, Y. and Bowers, Y.
Endocrine pancreas Consortium
Chipublished (2000)
Charler ESTS: inleb084.
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine pancreas Consortium
Harvard University, Howard Hughes Medical Institute
MA 02138
Fax: 617-4595-1812
Fax: 617-4595-1812
Fax: 617-4595-1812
Fax: 617-4595-1857
Email: dealtonebiohp, harvard.edu
Library was constructed by. Dr. J. Ferrer In vivo mass-excised to University Genome Sequencing Center For information on Charler Control PDNA sequencing by: Washington Clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
Seq Primer: -400P from Gibco
High quality sequence stop: 481.
Location/Qualifiers
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UI-HF-BLO-abu-e-01-0-UI.rl NIH-MGC_37 Homo sapiens cDNA clone
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Best Local Similarity 94.5%; Pred. No. 2.16-81;
Matches 308; Conservative 0; Mismatches 15; Indels 3; Gaps
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Euteleostomi;

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/organism="Homo sapiens"

/db xref="taxon:9666"
/clone="InAGE:5450551"
/clone="InAGE:545051"
/clone=
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                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-remail.inh.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov
Plate: LLCM1939 row: h column: 08
High quality sequence stop: 722.
Location/Qualifiers
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                                                                                                                                                                                                                                                                        NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 773)
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92.3%; Pred. No. 9.9e-78;
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                                                                    BM007845.1 GI:16522199
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Matches 301; Conservative
         mRNA sequence.
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AUTHORS
TITLE
JOURNAL
COMMENT
                                        ACCESSION
                                                                 VERSION
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Directionally cloned into BcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH MGC Library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BM007845 173 bp mRNA linear EST 30-OCT-2001 603617528F1 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5450551 5',
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                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 935)

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/clone="IMAGE:4575847"
/clone_lib="NIH MGC_48"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
                                                                                                                                                                                                                                                                                             Email: cgapDs-remmil.nih.gov
Tissue Procurement: louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1287 row: j column: 08
High quality sequence stop: 673.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
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In (bases 1 to 928)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: Capaba-remail.nih.gov

Tissue Procurement: Dr. Mark Matson

CDNA Library Preparation: Rubin Laboratory

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M. AG. E. Consortium (LINL)

DNA Sequencing by: Agencout Bioscience Corporation

Clone distribution: MGC clone distribution information can be http://image.llni.gov

Rubin A. Jissue Consortium/LLNL at:

Clone distribution: MGC clone distribution information can be http://image.llni.gov

Rubin: LLCMS517 row: 1 column: 14

High quality sequence stop: 651.
AGENCOURT_8475108 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6301597
50,0000 sequence.
BG7007369
BG707369.1 GI:21846268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 271.6; DB 14; Length 928;
Pred. No. 1.2e-76;
0; Mismatches 34; Indels 0;
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Best Local Similarity 89.6%;
Matches 292; Conservative
                                                                     human.
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Home sapiens

Bukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Merazoa; Chordata; Catarrhini; Hominidae; Homo.

The Sases I to 493; Primates; Catarrhini; Hominidae; Homo.

NIH-MGC http://mgc.nci.mih.gov/

NIH-MGC http://mgc.nci.mih.gov/

NIH-MGC http://mgc.nci.mih.gov/

Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Fasul: Capaba-romail.nih.gov

Eco RI site shown at the beginning of the sequence.

CDNA Library Preparation: M.B. Soares Lab

CONA Library Arrayed by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

CLOMA Library Arrayed by: M.B. Soares Lab

CLOME distribution: MGC clone distribution information can be

www-bio.lln.gov/bbrp//image/image/image.html

Seq primer: M13 Powaan: SoGG"

(Actione library MCG 37"

(Clone library MCG 37"

(Coll type="graminal center B cells"

(Abs. Factionally Cloned. Cells provided by Louis

M. Stadt, Ph.D. Library preparation by Maria de Patima

Bonaldo, Ph.D. and M. Bento Soares, Ph.D. "arrayed by MCG 31"

Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
AW405753 493 bp mRNA linear EST 16-FEB-2000 U-HF-BLO-abp-a-02-0-UI.rl NIH_MGC_37 Homo sapiens cDNA clone IMAGB: 3357290 5', mRNA sequence... AW405753 GI:6924810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         192 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGGTCCCATCA
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Best Local S:
Matches 298
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AUTHORS
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ORIGIN
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/clone_lib=NiH MGC 48"
/tissue_type="primary B-cells from tonsils (cell line)"
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/lab host="MiH MGC 48"
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/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5 adaptor: GGACGAGGG(0). Size-selected solobp for average insert size 1 8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
                                                    BG758398 921 bp mRNA linear EST 15-MAY-2001
602712592F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4852678 5',
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                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM697 row: h column: 23
High quality sequence stop: 848.
Location/Qualifiers
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Pred. No. 1.3e-75;
0; Mismatches 36;
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/db_xref="taxon:9606"
/clone="IMAGE:4852678"
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89.0%;
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Best Local Similarity 89.0%
Matches 290; Conservative
                                                                                                       mRNA sequence.
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                           #M407904
UI-HF-BLO-add-a-01-0-UI.K2 NIH_MGC_37 Homo sapiens cDNA clone
IMAGE:3061128 5', mRNA sequence.
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                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 422)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
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Bco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        db_xref="taxon:9666"
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AGENCOURT 6492277 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5589037 BM543718
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1 (bases 1 to 42.)

2 Yang, Y., Song, H., Peng, Y., Gu, Y., Gao, G., Xiao, H., Xu, X., Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Hu, R., Chen, J., Homo sapiens CDNA cdA clones

1 Unpublished (2000)

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1 Location/Qualifiers
                                                                                                             AV733746 AV33746 cdA Homo sapiens cDNA clone cdAATB08 5', mRNA sequence.
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118 c 117 g 99 t
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/organism="taxon:9606"
/clone="cdAdTB08"
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                        387 CCCGGGACCAAACTGGATATCAAACG 412
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| Ab xref="taxon:9606" |
| Ab xref="taxon:9606" |
| Clone="INAGE:5589037" |
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| Clone="INAGE:5589037" |
| Clone=Lib="NTH MGC_125" |
| Abb_host="DH10B" |
| Abb_host="Cryan : Ovary (pool of 3); Vector: pcMv-SPORT6; Site 1: EcoRV (destroyed); Site 2: Not!; RNA source pool of three ovaries, from females ranging in age from 38 to 49 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 2.1 kb, insert size range 1-3:5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 036:" |
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CE 1 (bases 1 to 1153)

RS NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

AL Unpublished (1999)

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Tissue Procurement: Invitrogen

CONTACT: Robert Straubardion: Life Technologies, Inc.

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81.1%; Score 265.2; DB 13; Length 1153;
Best Local Similarity 88.3%; Pred. No. 1.6e-74;
Matches 288; Conservative 0; Mismatches 38; Indels 0;
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AW404992 391 bp mRNA linear EST 16-FEB-2000 UI-HF-BLO-abx-a-03-0-UI.rl NIH MGC_37 Homo sapiens cDNA clone MAGE:3058060 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pT7T3-Pac; Site_1: Not1; Site_2: Eco RI; Constructed from size fractionated cytoplasmic mRNA [1.5-2.5kb]. Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180
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                                                                                                                                                                                                                     Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
Email: cgapbs.remail.nih.gov
Eco RI site showmal.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDM Library Preparation: M.B. Soares Lab
CDN Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GACATCCAGATGACCCAGTCTCCATCCTCTGTCTGCATCTGTAGGAGACAGAGTCACC
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                                                                                                                                                                                                                                                                                    1 (bases 1 to 391)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 80.6%; Score 263.6; DB 10; Length Best Local Similarity 90.2%; Pred. No. 2.8e-74; Matches 294; Conservative 0; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3058660"
/clone=lib="NIH_MGC_37"
/tissue='type='lymph"
/cell_type="garminal center B cells"
/cell_line="MGC85"
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KEYWORDS
SOURCE
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ORIGIN
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Search completed: July 18, 2003, 09:26:04 Job time: 568.66 secs

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8686.944 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES Description	ABK47275 Insulin-li					AAT88403 cDNA for anti-TNF-			
В	24 AI	24 AI	24 AJ	24 AJ		18 A			
% Query Match Length DB		761	752	752		321			
* Query Match]	93.2	91.3	90.3	90.3	90.3	85.4	85.0	84.5	
Score	304.8	298.4	295.2	295.2	295.2	279.2	278	276.4	
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CB2iE7 kappa light	Human anti-tumour	DNA encoding a sin	뎞	Humanised anti-Fas	Human IGFAM-1 immu	Human ovarian anti	. Antibody LD1-117-V	Nucleotide sequenc	Nucleotide sequenc	DNA sequence of li	TRO005.kappa chain	Sequence encoding	Anti-murine CTLA-4		Coding sequence fo	Anti-human AILIM m	Human anti-Rh(D) c	Human anti-Rh(D) c	Insulin/insulin-li	TRO005 kappa chain	Human anti-Rh(D) c	Human anti-Rh(D) a	Nucleotide sequenc	otide		antibod		Human coding seque	Human colon tumour	DNA encoding the k	드	Antibody ITA7 enco	Antibody ITA7 comp	Human endoglin (CD
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ALIGNMENTS

ABK47275 standard; DNA; 743 BP.

RESULT 1 ABK47275

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                                                                                                                        The invention relates to a method of modulating insulin activity in mammalian cells by adminstering a peptide that binds the insulin receptor (IR). A composition containing a peptide, optionally expressed from gene therapy vectors, that binds to Site 1 of IR and an insulin agonist are useful for treating diabetes. Also, peptides that are useful for treating diabetes. Also, peptides that are useful for treating insulin-like growth factor-1 (IGF-1) receptor are useful for treating insulin-like growth factor (IGF) sensitive tumours (e.g. of prostate and breast) and diabetic retinopathy, while IGF-1 receptor agonists are useful for treating neurological diseases, including stroke and diabetic neuropathy. The peptides are also useful in screening for compounds that bind to IR or IGF-1 receptor, potential therapeutics and research reagents. ABK47246-ABK47277 represent IR and/or IGF-1 receptor DNA sequences of the invention.
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                                        Modulating insulin activity in mammalian cells, for treating e.g. diabetes and tumours, comprises using peptides that bind to insulin or insulin-like growth factor receptors.
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93.2%; Score 304.8; DB 24; Length 743;
Best Local Similarity 98.5%; Pred. No. 4.5e-87;
Matches 319; Conservative 0; Mismatches 2; Indels 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Insulin/insulin-like growth factor receptor, DNA sequence #25.
                                                                                                                                                                                                                                                                                                                                Sequence 743 BP; 163 A; 195 C; 218 G; 167 T; 0 other;
                                                                                                  Disclosure; Figure 39; 390pp; English.
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               WPI; 2002-025774/03.
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241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a method of modulating insulin activity in mammalian cells by administering a peptide that binds the insulin receptor (IR). A composition containing a peptide, optionally expressed from gene therapy vectors, that binds to Site 1 of IR and an insulin adonist are useful for treating diabetes. Also, peptides that are useful for treating diabetes. Also, peptides that are useful for treating insulin-like growth factor-1 (IGF)-sensitive tumours (e.g. of prostate and breast) and diabetic retinopathy, while IGF-1 receptor agonists are useful for treating neurological diseases, including stroke and diabetic neuropathy. The peptides are also useful is creening for compounds that bind to IR or IGF-1 receptor, potential therapeutics and research reagents. ABRA1246-ABKA1277 represent IR and/or IGF-1 receptor DNA sequences of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      493 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                               Modulating insulin activity in mammalian cells, for treating e.g. diabetes and tumours, comprises using peptides that bind to insulin insulin-like growth factor receptors
                                                                                                                                                                                                                                                           Brandt J;
Mandecki WS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

91.3%; Score 298.4; DB 24; Length 761;
Best Local Similarity 97.2%; Pred. No. 5e-85;
Matches 315; Conservative 0; Mismatches 6; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 761 BP; 179 A; 201 C; 219 G; 162 T; 0 other;
                                                                                                                                                                                                                                                           Pillutla R, B:
Ostergaard S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Figure 19; 390pp; English.
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                                                                                                                                                                                                                                                           Schaeffer
J, Cheng
Hsiao K;
                                                                                                                                                                      (DGIB-) DGI BIOTECHNOLOGIES LLC (NOVO ) NOVO NORDISK AS.
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                                                                                                                29-MAR-2000; 2000WO-US08528
                                                      29-MAR-2000; 2000WO-US08528
                                                                                                                                                                                                                                                           Beasley J, Blume AJ,
Brissette R, Spetzler
Hansen PH, Ravera M,
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04-OCT-2001
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ng 664 GAAGATGTTGCAACTTACTGTCAAAGTATAACAGTGCCCCTTTCACTTTCGGC 720 301 CAAGGGACCAAGGTGGAATCAA 324 301 CAAGGGACCAAGGTGAATGAA 744 721 CCTGGAACAAAGTGAATTAAA 744	ABAY 12. ABAY 13. ABAY 12. ABAY 13. ABAY 12. ABAY 1
us-09-627-896b-25.rng	### STATE OF THE PROPERTY OF T

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and/or IGF-1 receptor DNA sequences of the invention.
                               Seguence 761 BP; 179 A; 200 C; 217 G; 165 T; 0 other;
                                                        Score 295.2; DB 24
Pred. No. 5.2e-84;
                                                          Query Match 90.3%; Score 295.2; Best Local Similarity 96.6%; Pred. No. 5.2e Matches 313; Conservative .0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                       301 CAAGGGACCAAGGTGGAAATCAAA 324
                                                                                                                                                                                                                                                                                                                                                                                                                         CCTGGGACCAAAGTGGATATCAAA 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAT88403 standard; cDNA; 321
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96US-0599226.
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P-PSDB; AAW27568.
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544 GGGAAAGTICCTAAGCICCTGAICTAIGCIGCAICCACTTIGCAAICAGGGGICCCAICT 603
                                                                                                                      604 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCAGC
                                                                                                                                                                          664 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCT---TACACTTTTGGC 720
                                             GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
                                                                                                   181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
                                                                                                                                                          241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modulating insulin activity in mammalian cells, for treating e.g. diabetes and tumours, comprises using peptides that bind to insulin insulin-like growth factor receptors
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Ostergaard S, Mandecki WS;
                                                                                                                                                                                                                                                                                                                                                                                                                              Cytostatic; antidiabetic; neuroprotective; cerebroprotective; ophthalmological; insulin; receptor; gene therapy; diabetes; insulin-like growth factor-1; IGF-1; tumour; prostate; breast; diabetic retinopathy; neurological diseases; stroke; diabetic neuropathy; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                      Insulin/insulin-like growth factor receptor, DNA sequence #30.
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                                                                                                                                                                                                                  CAAGGGACCAAGGTGGAAATCAAA 324
                                                                                                                                                                                                                                       721 CAGGGACCAAGCTGGAGATCAAA 744
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Brissette R, Spetzler J, Cheng W,
Hansen PH, Ravera M, Hsiao K;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                               ABK47276;
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                                                                                                                                                                                                                                                                                        RESULT 5
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                                                                                                                                                                                                                                                                                                                               61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
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                                                                                                                                                               1 GACATCCAGATGACCCAGTCTCCATCCTCCTGTTCTGCATCTAGGAGACAGAGTCACC
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                                                                                      3,
DB 24; Length 761;
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Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P;
Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA for anti-TNF-alpha antibody light chain variable region.
                                                                                  8; Indels
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Query Match 85.0%; Score 278; DB 24; Length 632; Best Local Similarity 92.9%; Pred. No. 1.5e-78; Matches 303; Conservative 0; Mismatches 20; Indels 3
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                                                                                                                               factor-alpha (TNF-alpha) antibody (Ab) light chain variable region.

The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or less and has a Koff rate constant of 1x10 power -3 s power -1 or less (both determined by surface plasmon resonance), and neutralises human TNF-alpha cytotoxicity in a standard in vitro is 1929 assay with an ICSO of 1x10 power -7 M or less. The Ab, which inhibits TNF-alpha activity, can be used to treat sepsis, autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid arthritis, spondylitis, osteoarthritis, gouty arthritis, allergy, multiple sclerosis, autoimmune diseases, malagnancy, pulmonary, intestinal, cardiac or inflammatory bone disorders, bone resorption disease, alcoholic, viral or fulminant hepatitis, coaquiation disturbances, burns, reperfusion injury, Reloid formation, scar tissue formation, pyrexia, periodontal disease, obesity and radiation toxicity. The below of inhibits TNF-alpha induced expression of endothelial cell invocate abbesich was made of endothelial cell invocate abbasic of inhibits TNF-alpha induced expression of endothelial cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                finity antibodies against human TNF alpha - useful to inhibit
na activity, e.g. to treat autoimmune diseases and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antibody, Cgamma, Ckappa, Clambda2, ds, transgenic; vector, infectious disease, malignancy, cancer; tumour, autoimmune disease, humanised immunoglobulin; cytostatic; antibacterial; virucide, fungicide; light chain variable region; heavy chain variable region;
                                                                                                                     anti-human tumour necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                               on human umbilical vein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 18; Length 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 85.4%; Score 279.2; DB 18; Local Similarity 93.5%; Pred. No. 4.8e-79; nes 303; Conservative 0; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 321 BP; 85 A; 87 C; 74 G; 75 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human/rabbit Ckappa chimaeric DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             eukocyte adhesion molecule-1 (ELAM-1)
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                                                                                                                     sequence encodes a novel
                                                                             Disclosure; Page 75; 102pp; English
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              High affinity antibodies
TNF alpha activity, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  endothelial cells (HUVEC)
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transgenic animal, comprising a numanised immunoglobulin prelates to a numanised immunoglobulin dearlyed invention relates to a numanised immunoglobulin of a human immunoglobulin colypeptide sequence (e.g. form immunoglubulin Cgamma, Ckappa or clambda2). Also included area 1) nucleic acid molecules comprising the clambda2). Also included area 1) nucleic acid molecules comprising the creation of rabbit Cgamma, the 3' flanking the creation of rabbit Cgamma, the 3' flanking regions of cow, sheep and rabbit Cgamma, the 3' flanking region of rabbit Cgamma, cc 2) a recombination vector for replacing an If gene segment from a non-human animal with a human immunoglobulin (Ig) gene segment, cc comprising from 5' to 3', a 5' nucleotide sequence, the human ig gene segment, and a 3' nucleotide sequence, where the 5' and 3' nucleotide sequence, or a nucleotide sequence, or a sequence, or an unimal sequence of the gene sequence, and the locus or sequences of the gene sequence of the gene sequence of the gene sequence of the gene sequence or an autoimmune disease in the non-human animal and 3) a transgenic or an autoimmune disease in the non-human animal and 3) a transgenic or an autoimmune disease in contaminal and and producing a the construct into a recipient cell or non-human animal and an introducing the construct into a recipient cell or a non-human animal and an impaired expression of endogenous Ig molecules, and the recipient cell is a fertilised egg. Humanised antibodient cell is a setul fer recipient cell is a setulised egg. Alternat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel humanised antibodies useful for treating diseases caused bacterial, viral, fungal infection and cancer, are derived from transgenic non-human animals engineered to contain humanised
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              humanised heavy or light chains, respectively are mated and an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a humanised immunoglobulin derived
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Platzer J, Buelow J;
Chimeric - Oryctolagus cuniclus.
Chimeric - Homo sapiens.
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15-MAR-2001; 2001US-276156P.
                                                                                                                                                                                                                                                                                                                                            03-AUG-2001; 2001WO-US24348.
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PLATZER J.
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2 ACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCA 61

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                                               GGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTTACCATCAGCAGCCTGCAGCCTG
                                                                                                                                                                                  GGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCTC
                                                                                                   GGAAGGTTCCCAAGCTCCTGATTTATGCTGCATCCACTTTGCAATCTGGGGTCCCATCGC
                                                                                                                          GGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic acid that is differentially expressed in cancer tissues useful for determining the presence of colon cancer in a cell or tissue type, and in antisense therapy
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                                                                                                                                                                                                                                                                                                                                                                Human colon cancer related nucleotide sequence SEQ ID NO:2618.
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Thiaglingam A, Lewis ME;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, pancreatic tumour protein; pancreatic cancer; therapy; diagnosis; cancer; vaccine; cytostatic; ss.
corresponding gene resides, and in tissue profiling, forensics, genetic analysis, mapping and diagnostic applications. (I) can be used to raise antibodies, and to screen for peptide analogues and antagonists.
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                                                                                                                                                                                                                                                                                                                                                                              104 GACATCCAGATGACCCCAGTCTCCATCTTTCCTGTCTGCATCTGTAGGAGACAGAGTCACCC
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                                                                                                                                                                                                          DB 24; Length 565;
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                                                                                                                                                                                                  Query Match 84.5%; Score 276.4; DB 24; Length Best Local Similarity 92.6%; Pred. No. 4.6e-78; Matches 302; Conservative 0; Mismatches 21; Indels
                                                                                                                                         Sequence 565 BP; 128 A; 155 C; 142 G; 134 T; 6 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAGGGGACCAAGTTGGAGATCAAACG 426
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relater, to therapy and diagnosis of cancer, such as pancreatic cancer. The polypeptides and polymucleotides of the invention are useful as vaccines and pharmaceutical compositions for preventing and treating pancreatic cancer, as well as for the diagnosis and monitoring of such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neuromodulatory; central nervous system; CNS; sHIGM22; LYM 22; AKJR4; ebvHigM MsI19D10; ebv HIGM CB2bG8; CB2iE12; CB2iE7; MSI19E5; virucide; antiparkinsonian; neuroprotective; nootropic; vulnerary; ds.
                                                                                                                                                                                                              GACATCCAGATGACCCCAGTCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC
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                                                            cancers. The present sequence is human pancreatic tumour protein
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                                                                                                                                  DB 24; Length 737;
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                                                                                                                                                                32; Indels
                                                                                                     Sequence 737 BP; 188 A; 211 C; 181 G; 153 T; 4 other;
                                                                                                                                  Score 274.8; DB 2
Pred. No. 1.7e-77;
                                                                                                                                                                 0; Mismatches
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                                                                                                                                  84.0%;
90.2%;
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                                                                                                                                                                294; Conservative
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                                                                                                                                                  Local Similarity
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P-PSDB; ABB07183
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The invention provides a neuromodulatory agent (I) capable of promoting neurite outgrowth, regeneration, remyelination and neuroprotection in central nervous system (CNS). (I) is capable of inducing remyelination, promoting cellular proliferation of glial cells, and promoting Ca2+ signaling with oligodendrocytes. An humanised antibody to (I) can be selected from antibody sHIGMSZ (LMW 22), ebvHigh Ms11910, ebv High CG2268, AKMR4, CB31B12, CB21E7 or MS119E5. (I) is useful for stimulating cremyelination of CNS axons, or treating demyelinating proliferation of glial cells in CNS axons, or treating demyelinating disease of CNS in a mammal in need of such therapy. (I) is capable of binding to structures and cells within CNS. (I) is preferably useful for treating a demyelinating disease of CNS of a mouse infected with Strain DA of Theller's mutine encephalomyelitis (TMEV) or for treating a human being having multiple sclerosis, or a chuman or domestic animal with a viral demyelinating disease of CNS. (I) is also useful for simulating remyelination of CNS axons. The stimulating the proliferation of glial cells from mixed cell culture. (I) is also useful for stimulating remyelination of CNS axons. The antibodies are useful for preventing infection by a bacterium, virus or like pathogen that causes demyelination or other neurodegenerative condition in a subject. Methods where (I) is administered to a patient are useful for treating multiple sclerosis, parkinson's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arcactrocogocoagreagocarrageaarrarragecrograreagoaaaacea 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alzheimer's disease, amyotrophic lateral sclerosis (ALS), a viral demyelinating disease, CNS diseases, and other conditions in the CNS where nerves are damaged as by trauma. The present sequence represents the CB2iE7 kappa light chain variable region nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 CGGTTCAATGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAACCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 24; Length 306;
Novel neuromodulatory agent (a human IgM monoclonal antibody) promoting neurite outgrowth, regeneration, remyelination and neuroprotection in central nervous system, useful to treat post-infectious encephalomyelitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83.9%; Score 274.4; DB 24;
llarity 97.9%; Pred. No. 1.6e-77;
Conservative 0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 306 BP; 77 A; 84 C; 70 G; 75 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human IGFAM-10 immunoglobulin coding sequence
                                                                                                                             42; 219pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAA27390 standard; cDNA;
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Matches 278; Conserv
                                                                                                                          Claim 43; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
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241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAAAGTGCCCCCTCCGAGTACGTTCGGC 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 ATCACTTGCCGGGGGGGGGGGGGGTTAGCATTATTTAGCCTGGTATCAGCAGAAACCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anticancer human monoclonal antibody variable region sequences - and related DNA and RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human anti-tumour antigen antibody light chain variable region cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, tumour antigen, cancer, monoclonal, antibody, light chain, variable region; medicine; pharmacology; biochemistry; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence encodes a human anti-tumour antigen monoclonal antibody (MAD) light chain variable region, useful medicine, pharmacology and biochemistry. The isotype of a MAD secreted by the human/human hybridoma HT was determined to be and kappa. Human MAD was purified, and the antigen recognised human MAD was purified, and the antigen recognised human MAD cLN*_ISM identified by western blocting.
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82.6%; Score 270; DB 18; Length 396;
Best Local Similarity 91.4%; Pred. No. 4.5e-76;
Matches 298; Conservative 0; Mismatches 25; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 396 BP; 101 A; 107 C; 97 G; 91 T; 0 other;
                                                                                                              CAAGGGACCAAGGTGGAAATCAAACG 326
                                                                                                                                                                    caaggacacacregagarraaacg
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                                                                                                                                                                                                                                                                                                                        BP
                                                                                                                                                                                                                                                                                                                        AAT75423 standard; cDNA; 396
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/*tag= 6
67..396
/*tag= 1
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                                                                                                                                                                                                                                              RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A CGTTCAGTGGCAGTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           145 ATCACTTGCCGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is the human immunoglobulin superfamily protein IGFAM-10 gene, which was isolated from a cDNA library of colon tissue. It is expressed in reproductive, gastrointestinal and cardiovascular tissue, where cancer and inflammation are common. The gene, protein, its antibodies, agonists and antagonists are suitable for diagnosing and treating many diseases, including cancer, immune system disorders (such as inflammation, AIDS, allergies, anemia, arterioscierosis, asthma, atheroscierosis, cholecystitis, Crohn's disease, diabetes mellitus, emphysema, Graves' disease, hepatitis, multiple sclerosis, psoriasis, rheumatoid arthritis, scleroderma, systemic lupus erythematosus and ulcerative collitis), complications of cancer, haemodialysis and extracorporaal circulation, trauma and haematopoietic cancer (such as leukaemia) and infections caused by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunoglobulin superfamily proteins, the agonist and antagonist of the protein is useful for preventing and treating disorders associated with altered levels of the protein such as cancer, immune system disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        265 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
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B3.1%; Score 271.6; DB 21; Length 936;
Bert Local Similarity 89.6%; Pred. No. 1.99-76;
Matches 292; Conservative 0; Mamatches 34; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gorgone GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 936 BP; 239 A; 276 C; 214 G; 207 T; 0 other;
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Yang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bacteria, viruses, fungi or parasites.
                                                                                                              /*tag= a 'IGFAM-10" | product= "IGFAM-10" | 19..84 | k-tag= b | k-tag= c | /*tag= c | /*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 9; Page 99-100; 105pp; English.
                                                     Location/Qualifiers
19..732
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98US-0113635.
99US-0128194.
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Lal P, Hillman JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-US27566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (INCY-) INCYTE PHARM INC.
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P-PSDB; AAY96298.
                                                                                                                                                                                                                                                                                                                        WO200029583-A2
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22-DEC-1998;
07-APR-1999;
   sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                       19-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                 25-MAY-2000
                                                                                                                                                                           sig_peptide
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GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCTCAG---ACGTTCGGC 363
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                     247 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT
                                                                     GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC
                                                                                                                                                                                                                                                                                                                                                                                                 Screening; functional polypeptide; ligand; non-functional; enrichment; single chain antibody; ScFv; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Screening for functional polypeptides which bind a ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 720 BP; 168 A; 181 C; 214 G; 157 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                DNA encoding a single chain antibody (ScFv).
                                                                                                                                                            CAAGGGACCAAGGTGGAAATCAAACG 389
                                                                                                                                       CAAGGGACCAAGGTGGAAATCAAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 2; 67pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97GB-0022131.
                                                                                                                                                                                                                                                          AAX36070 standard; DNA; 720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97US-0066729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MEDI-) MEDICAL RES COUNCIL
                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tomlinson I, Winter G;
                                                                                                                                                                                                                                                                                                                                                                                                Screening, functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-288302/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9920749-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-OCT-1997;
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397 GACATCCAGATGACCCAGTCTCCATCCTCCTGTCTGCATCTGTAGGAGACAGAGTCACC 456

1 GACATCCAGATGACCCAGTCTCCATCCTCCTGTCTGCATCTGTAGGAGACAGAGTCACC

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Gaps

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25; Indels

DB 20; Length 720;

82.6%; Score 270; DB 20; 91.4%; Pred. No. 5.6e-76; ive 0; Mismatches 25

Local Similarity 91.4 les 298; Conservative

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Query Match Best Local 8 Matches 298

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Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic; dernatological; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; nephrotropic; antiinfertility; neuroprotective; antiarteriosolerotic; heparotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; multiple syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosolerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection; ss.
                                                                  180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral,
                                                                                                                                                                                                                                  457 ATCACTIGCCGGGCAAGICAGAGCATIAGCAGCIATITAAATIGGTAICAGCAGAAACCA
                                                                                                     517 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA
                                                                                                                                                            AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
                                                                                                                                                                                                            241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC
                                                                    GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT
                                                                                                                                        181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New humanized anti-Fas antibody, useful for treating or preventing inflammatory or autoimmune disease, induces apoptosis selectively i cells with abnormal Fas-Fas ligand systems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human immunoglobulin light chain kappa region subgroup type I DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Takahashi T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tamaki I,
                                                                                                                                                                                                                                                                                                          CAAGGGACCAAGGTGGAAATCAAACG 719
                                                                                                                                                                                                                                                                                  CAAGGGACCAAGGTGGAAATCAAACG 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nakahara K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2; Page 154; 263pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                           AAA11630 standard; DNA; 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99EP-0307711.
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98JP-0276882.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Haruyama H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SANY ) SANKYO CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-258930/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-AUG-2000
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28-MAR-2001; 2001JP-0093106. 29-MAR-2000; 2000JP-0090918, (SANY) SANKYO CO LTD. WPI; 2002-145113/19.

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Immunoautiacty, dermatological, immunoauppessive, chyronimetic, antitrheumatic, nephrotropic, antiinfertility, neuroprotective, chimbibit of ligand binding to cell surface Fas or inhibit it by competitive inhibit and binding to cell grades associated with the Fas/Fas ligand system, capecially systemic lupus erythematosus, Hashimoto disease, pernicious or hypoplastic versus host disease, Slorgen's syndrome, pernicious or hypoplastic camemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease, autoimmune hemolytic anemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin capented in allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminat, chronic, viral (B, C or D) or alcoholic), and transplant rejection. (I) selectively inhibit apoptosis in normal cells but selectively induce it in abnormal cells used murine fas, so can be evaluated in continuing a human anti-murine antibody response. This sequence represents inducing a human anti-murine antibody response. This sequence represents a human immunoalpolulin light chain kappa variable region subgroup type I which is used in the construction of humanised anti-Fas antibody constructs described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73 GACATCCAGATGACCCAGTCTCCATCCTCCTGTCTGCATCTGTAGGAGACAGAGTCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGGAAAGTICCIAAGCICCIGAICIAIGCIGCAICCACITIGCAAICAGGGGICCCAICI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, mouse, humanised anti-Fas antibody, Fas/Fas ligand,
light chain subunit; apoptosis; immunosuppressive; antiallergic;
autoimmune disease; allergy; atopic; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 270; DB 21; Length 729;
Pred. No. 5.6e-76;
0; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Humanised anti-Fas antibody related PCR primer SEQ ID NO 76,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 729 BP; 192 A; 200 C; 182 G; 155 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABL46009 standard; DNA; 729 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 82.6%;
Best Local Similarity 91.4%;
Matches 298; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                       GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
                                                                                                                                                                                                                                                                                                                                                                                                                313 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCTC---GAACGTTCGGC 369
                                                                                                                                                                                                                                GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
                                                                                                                                                                                                                                                         GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCTTGCAAGTGGGGTCCCATCA 252
                                                                            9
                                                                                                  GACATCCAGATGACCCAGTCTCCATCCTCCTCTGCATCTGTAGGAGACAGAGTCACC
                                                                            GACATCCAGATGACCCAGTCTCCATCCTCTGTGTCTGCATCTGTAGGAGACAGAGTCACC
                                                                                                                                                                                                                                                                                                             181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT
                                                                                                                                                        ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA
                                        Gaps
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Query Match
82.6%; Score 270; DB 24; Length 729;
Best Local Similarity 91.4%; Pred: No. 5.6e-76;
Matches 298; Conservative 0; Mismatches 25; Indels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAAGGGACCAAGGTGGAAATCAAACG 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: July 18, 2003, 06:44:04 Job time : 86.7713 secs
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The invention relates to a preventive or treating agent for diseases caused by a bnormality in Fas/Fas ligand system containing as the active component an antibody having as the light chain subunit a polypeptide containing residues 1-218 of one of 3, 239 residue amino acid sequences, or residues 1-451 of one of 3, 470 residue amino acid sequences, dully defined in the specification and having an activity of combining specifically with mammalian Fas and an activity of induring appropriation a cell expressing Fas. The agent has immunosuppressive and alseases, allergy, alopy and is used for preventing and treating autoimmune pCR primer, useful to the invention.

Sequence 729 BP; 192 A; 200 C; 182 G; 155 T; 0 other;

nsed for

Example 15 (Preparatory); Page 40; 194pp; Japanese. Drug containing humanised anti-Fas antibody, user treating autoimmune diseases, allergy, and atopy

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM nucleic - nucleic search, using sw model Run on:

July 18, 2003, 06:19:39; Search time 79.0498 Seconds (without alignments) 8533.875 Million cell updates/sec

1 gacatccagatgacccagtc......... US-09-627-896B-25 327 Perfect score: Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

1439767 seqs, 1031500376 residues Searched:

Total number of hits satisfying chosen parameters:

2879534

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published Applications NA:*

1: /cgn2 6/ptodata//pubpna/US07 PUBCOMB.seq:*

2: /cgn2 6/ptodata//pubpna/DS07 NEW PUB.seq:*

3: /cgn2 6/ptodata//pubpna/US06 NEW PUB.seq:*

4: /cgn2 6/ptodata//pubpna/US06 PUBCOMB.seq:*

5: /cgn2 6/ptodata//pubpna/US06 PUBCOMB.seq:*

6: /cgn2 6/ptodata//pubpna/US08 NEW PUB.seq:*

7: /cgn2 6/ptodata//pubpna/US08 NEW PUB.seq:*

7: /cgn2 6/ptodata//pubpna/US09 NEW PUB.seq:*

9: /cgn2 6/ptodata//pubpna/US09 NEW PUB.seq:*

10: /cgn2 6/ptodata//pubpna/US09 NEW PUB.seq:*

11: /cgn2 6/ptodata//pubpna/US09 NEW PUB.seq:*

12: /cgn2 6/ptodata//pubpna/US09 NEW PUB.seq:*

13: /cgn2 6/ptodata//pubpna/US09 NEW PUB.seq:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result	Ļ		Query					
Ž	No.	Score	Match	Match Length DB	DB	ID	Description	
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	н	294	89.9	514	15	US-10-066-543-2025	Sequence 2025, Ap	
υ	7	294	89.9	537	15	US-10-066-543-186	Sequence 186, App	
	m	279.2	85.4	321	12	US-09-801-185A-36		
	4	278	85.0	490	12	US-09-918-995-37859	Sequence 37859, A	
	S	274.8	84.0	737	11	US-09-919-344-7	Sequence 7, Appli	
	9	274.8		819	15	US-10-158-646-65	ဖ	
	7	270		720	10	US-09-192-854-1		
	8	270		720	11	US-09-968-561A-1		
	თ	270	82.6	729	15	US-10-216-484-125		
	20	264.8	81.0	321	15	US-10-035-637-1		
	11	263.6	90.6	974	11	US-09-859-053-29	Sequence 29, Appl	
	12	263.4	80.6	324	12	US-09-848-798-101		
	13	263.4	90.6	324	12	US-09-848-798-112	Sequence 112, App	
	14	261.8	80.1	324	12	US-09-848-798-110	110,	
	15	261.8	80.1	324	12	US-09-848-798-210		
	16	260.4	79.6	326	10	US-09-798-058-3	3, Apı	

GACATCCAGATGACCCAGTCTCCATCCTCCCTGCTTGCATCTGTAGGAGACAGAGTCACC 137 61 ATCACTTGCCGGGCGAGTCAGGCCATTAGCAATTATTAGCCTGGTATCAGCAGAAACCA 120

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1 GACATCCAGATGACCCAGTCTCCATCCTCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60

89.9%; Score 294; DB 15; Length 514; 96.0%; Pred. No. 8.2e-92; ive 0; Mismatches 10; Indels

Query Match 89.9 Best Local Similarity 96.0 Matches 313; Conservative

Gaps 3;

Sequence 1811, Ap Sequence 1811, Ap Sequence 1811, Ap Sequence 15, Appl Sequence 15, Appl Sequence 224, Appl Sequence 224, Appl Sequence 13, Appl Sequence 13, Appl Sequence 218, Appl Sequence 218, Appl Sequence 222, Appl Sequence 221, Appl Sequence 221, Appl Sequence 221, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 18784, Appl Sequence 18784, Appl Sequence 20, Appl	ednence ednence ednence ednence
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ALIGNMENTS

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APPLICANT: Fanger, Gary R.
APPLICANT: Smith, Carole L.
APPLICANT: Smith, Carole L.
APPLICANT: Surth, Margarita
APPLICANT: Stolk, John A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REPERENCE: 210121.53
CURRENT APPLICATION NUMBER: US/10/066,543
CURRENT FILING DATE: 2002-01-31
NUMBER OF SEQ ID NOS: 3417
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2025
LENGTH: 514
Sequence 2025, Application US/10066543 Publication No. US20030087818A1 GENERAL INFORMATION:
                                                                                   APPLICANT: Jiang, Yuqiu
APPLICANT: Pyle, Ruth A.
APPLICANT: Yu, Jiangchun
APPLICANT: Indirias, Carol Yoseph
                                                                                                                                                                                          Lodes, Michael J
                                                                                                                                                                                                                      Secrist, Heather
                                                                                                                                                                                                                                               Carter, Darrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
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121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
121 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
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197 GAAGATGTTGCAACTTATTTCTGTCAAAAATATAACAGTGCC---CCCGGGACGTTCGGC
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US-09-801-185A-36
US-09-801-185A-36
Sequence 36, Application US/09801185A
Publication No. US20030092059A1
GENERAL INFORMATION:
APPLICANT: BASF Aktiengesellschaft
TITLE OF INVENTION: Human Antibodies that Bind Human TNFalpha
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 28 SCACE ...
CITY: BOSTON
STATE: Massachusetts
COUNTRY: USA
ZITE: 0109
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09/801,185A
FILING DATE: 07-Mar-2001
PRIOR APPLICATION NUMBER: US 08/599,226
FILING DATE: 09-FEB-1996
APPLICATION NUMBER: US 06/031,476
FILING DATE: 07-MG-1998
APPLICATION NUMBER: US 06/031,476
FILING DATE: 07-MG-1998
APPLICATION NUMBER: US 09/125,098
ATTORNEY AGENT INFORMATION:
NAME: DECORTI Giulio A., Jr.
REGISTRATION NUMBER: 31.03
REPERRENCE/DOCKET NUMBER: BBI-043CPUSCN
TELEPHONE: (617)227-7400
TELEPHONE: (617)227-7400
TELEPHONE: (617)227-5941
INFORMATION FOR SEE
SEQUENCE CHARACTERISTICS:
LEMOTH: 321 base pairs
TVPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

85.4%; Score 279.2; DB 12; Length
Best Local Similarity 93.5%; Pred: No. 9.4e-87;
Matches 303; Conservative 0; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ 1D NO: 36:
US-09-801-185A-36
                                                                                                              140 CAAGGGACCAAGGTGGACATCAAACG 115
                                                                                  301 CAAGGGACCAAGGTGGAAATCAAACG 326
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31.7 GGAAAGTTCCTAAGCTCCTGATCTATGCTGCATTTGCAATCTGGGGTCCCATCT 258
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   138 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 197
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                                                                                                     198 GGAAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCTGGGGGTCCCATCT 257
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GUREMAL INVENTATION:

APPLICANT: Pyle, Ruth A.

APPLICANT: Pyle, Ruth A.

APPLICANT: Pyle, Ruth A.

APPLICANT: Indirias, Carol Yoseph

APPLICANT: Indirias, Carol Yoseph

APPLICANT: Gecrist, Heather

APPLICANT: Gerrer, Darrick

APPLICANT: Gary R.

APPLICANT: Smith, Carole L.

APPLICANT: Smith, Carole L.

APPLICANT: Scolk, John A.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTIONS AND METHODS FOR THE THERAPY
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                                                     GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTT
                                                                                                                                                                                                                                                                                                                                                                                  CAAGGGACCAAGGTGGAAATCAAACG 326
                                                                                                                                                                                                                                                                                                                                                                                                                                  CAAGGACCAAGGTGGACATCAAACG 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 186, Application US/10066543; Publication No. US20030087818A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: n = A,T,C or G
US-10-066-543-186
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ORGANISM: Homo sapiens
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LOCATION: 529
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144 ATCACTIGCCGGGCGAGTCAGGGCATTAGCAATTCTTTAGCCTGGTATCAGCAGAAACCA 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              324 GAAGATTTTGCAACTTATTACTGTCAACAGTATTATAGTAACCCTCCGGTCACTTTCGGC 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT
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84.0%; Score 274.8; DB 11; Length 737;
Best Local Similarity. 90.2%; Pred: No. 4.4e-85;
Matches 294; Conservative 0; Mismatches 32; Indels 0;
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER FILE REPRENEUS: 210121.1.43
CURRENT APPLICATION NUMBER: US/09/919,344
CURRENT FILING DATE: 2001-07-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 77
LENGTH: 737
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OTHER INFORMATION: Incyte ID No. US20030073105A1 1329729.1
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Publication No. US20030073105A1

GENERAL INPORMATION:

APPLICANT: Lasek, Amy K W.

TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER

FILE REFERENCE: PA-0030-1 US

CURRENT APPLICATION NUMBER: US/10/158,646

CURRENT FILING DATE: 2002-05-29

PRIOR FILING DATE: 2001-05-31

NUMBER OF SEQ ID NOS: 78

SOFTWARE: PERL PROGRAM

SEQ ID NO 65

LENGTH: 819
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                   TYPE: DNA
                                                                                                                                                                                                                                                                                 FEATURE:
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                                                                             GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
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  180 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAGTTACTTAGCCTGGTATCAGCAGAAACCA
                                                                                                                              241 GAAGATGTTGCAACTTATTACTGTCAAAGGTATAACCGTG---CACCGTATACTTTTGGC
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APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: EROW VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-75
CURRENT APPLICATION UNMBER: US/09/918,995
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/215,076
PRIOR PILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOUTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/09919344
Patent No. US20020137911A1
GENERAL INFORMATION:
APPLICANT: Pyle, Ruth A.
APPLICANT: Xu, Jiangchun
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Matches 303, Conservative
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ORGANISM: Homo sapiens
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180

120

Gaps

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323

Gaps

us-09-627-896b-25.rnpb

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Sequence 125, Application US/10216484
Publication No. US20030103976A1
GENERAL INFORMATION:
APPLICANT: Berizawa, No. US20030103976A1ufusa
APPLICANT: Haruyama, Hideyuki
APPLICANT: Tamaki, Ikuko
TITLE OF INVENTION: Anti-Fas Antibodies
FILE REFERENCE: 980126CIP/HG
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US-09-968-561A-1
                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
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                   ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA
                                                                                                                                      206 GGGACAGCCCCTAACCTCCTGATCTATGGTGCATCCACTTTGCAATCAGCTGTCCCATCT
GACATCCAGATGACCCAGTCTCCATCTCCTGCTTGCATCTGTAGGAGACAGAGTCACC
                                                                                                                    GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT
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; Sequence 1. Application US/09192854
; Patent No. US2002068276A1
; GENERAL INFORMATION:
   APPLICANT: Winter, Greg
; APPLICANT: Winter, Greg
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
; CURRENT FILING DATE: 1998-11-17
; EARLIER FILING DATE: 1998-11-17
; MUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
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; ORGANISM: Homo sapiens
US-09-192-854-1
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Sequence 1, Application US/09968561A

Sequence 1, Application US/09968561A

Patent No. US20020164642A1

GENERAL INFORMATION:
APPLICANT: Tomilnson, Ian M

APPLICANT: Winner, Gregory

TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands

FILER REFERENCE: 8039/1073B

CURRENT APPLICATION NUMBER: US/09/968,561A

PRIOR APPLICATION NUMBER: US 60/065,248

PRIOR APPLICATION NUMBER: US 60/066,729

PRIOR PILING DATE: 1997-11-21

PRIOR PELING DATE: 1997-11-21

PRIOR PELING DATE: 1998-10-20

PRIOR PELING DATE: 1998-10-20

PRIOR PELING DATE: 1998-10-20

PRIOR SED IN OND ATE: 1998-10-20

PRIOR APPLICATION NUMBER: US 60/066,729

PRIOR PELING DATE: 1998-10-20

SOFTWARE OF SEC ID NOS: 350

SOFTWARE: PatentIn Version 3.1

LENGTH: 720
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191 ACATCCAGATGACCCAGTCTCCATCCTGTTGCATCTGTAGGAGACAAAGAACAGATCACC
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82.6%; Score 270; DB 11; Length 720;
Best Local Similarity 91.4%; Pred. No. 2e-83; Indels
Matches 298; Conservative 0; Mismatches 25; Indels
CAAGGGACCAAGGTGGAAATCAAACG 719
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61 ATCACTTGTCGGGGGGGGTATTAGCAGGTGGTTAGCCTGGTATCAGCAGAAAACCA 120
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APPLICANT: TSUJI, NO. US202020102658Aluaki
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
FILE REFERENCE: 06501-07901
CURRENT APPLICATION NUMBER: US/09/859,053
CURRENT FILING DATE: 2001-05-16
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: UP 2001-147116
PRIOR FILING DATE: 2000-05-18
                                                                                 1 GACATCCAGATGACCCAGTCTCCATCTCACTGTCTGCATCTGTAGGAGACAGAGTCACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC
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Pred. No. 3.8e-81
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       Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
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90.2%;
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Best Local Similarity 90.23
Matches 294; Conservative
       294; Conservative
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LOCATION: (39):..(104)
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LENGTH: 974
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Publication No. US20030031667A1
GENERAL INPORMATION:
APPLICANT: Dec, Yashwart M.
APPLICANT: Eder, Tibor
TILLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO DENDRITIC
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO DENDRITIC
TITLE OF INVENTION: HUMAN MAIL OF SET STATES TO THE SEPRENCE: MXI-166CP
CURRENT PAPLICATION NUMBER: US/10/035,637
CURRENT FILING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: 09/851,614
PRIOR APPLICATION NUMBER: USSN 60/203,126
PRIOR APPLICATION NUMBER: USSN 60/203,739
PRIOR FILING DATE: 2000-05-08
PRIOR PELING DATE: 2000-09-07
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FASTESEQ for Windows Version 4.0
LENGTH: 321
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Pred. No. 9.5e-82;
                                                                                                                                                                                                                                                                                                           Length 729;
                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                           Score 270; DB 15;
Pred. No. 2e-83;
0; Mismatches 25;
         CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US/09/499,662
PRIOR FILING DATE: 2000-02-09
PRIOR FILING DATE: 1998-04-01
NUMBER OF SEQ ID NOS: 165
LENGTH: 729
CURRENT APPLICATION NUMBER: US/10/216,484
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90.7%;
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Best Local Similarity 91.4%;
Matches 298; Conservative
                                                                                                                                                                                                           ; TYPE: DNA
; OkGANISM: Homo sapiens
US-10-216-484-125
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; LOCATION: (1)...(321)
US-10-035-637-1
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Best Local Similarity
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US-09-848-798-101
US-08-84-708-101
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US-08-88-708-101
US-08-88-708-105-101
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US-08-88-708-105-101
US-08-88-708-101
US-08-8
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181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCT 240
285 AGGTTCAGCGGAGAGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 344
                                                                                                                                                                                                                                                               241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300 345 GAAGATTTTGCAACTTACTATTGCCAACAGGCTAACAGTTTC---CCGTGGACGTTCGCG 401
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80.6%; Score 263.4; DB 12; Length
Best Local Similarity 88.8%; Pred. No. 2.9e-81;
Matches 285; Conservative 0; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                    301 CAAGGACCAAGGTGGAAATCAAACG 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                             402 CAAGGGACCAAGGTGGAAATCAAACG 427
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; OTHER INFORMATION: anti-Rh(D) chain 101
S.09-848-101
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ORGANISM: Homo sapiens
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Sequence 112, Application US/09848798
; Sequence 112, Application US/09848798
; Publication No. US20030040605A1
; FUBLICANT: Siegel, Donald I.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798'
; CURRENT APPLICATION NUMBER: DALLIER APPLICATION NUMBER: 09/240,274
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR PILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SEQ ID NO 112
; LENGTH: 324
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80.6%; Score 263.4; DB 12; Length 324;
Best Local Similarity 88.8%; Pred. No. 2.9e-81;
Matches 285; Conservative 0; Mismatches 36; Indels 0;
                                                                                                                                                                                                                                                                                                                                     ), OTHER INFORMATION: anti-Rh(D) chain I12
US-09-848-798-112
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ORGANISM: Homo sapiens
FEATURE:
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Sequence 210, Application US/09848798

Publication No. US2030040665A1

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: Bh(D) - BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL

TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF

TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF

FILE REPRENCE: 05596-4202

CURRENT APPLICATION NUMBER: US/09/848,798

CURRENT FILING DATE: 2001-05-04

PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29

PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11

NUMBER OF SEQ ID NOS: 224

SOFTWARE: PATENTIN VAR. 2.0

SEQ ID NO 210

LENGTH 3.24
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US-09-848-798-210
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Pred. No. 1.1e-80;
0; Mismatches 37
                                                                                      Query Match 80.1%; Score 261.8; DB 1
Best Local Similarity 88.5%; Pred. No. 1.1e-80;
Matches 284; Conservative 0; Mismatches 37
                                ; OTHER INFORMATION: anti-Rh(D) chain I10
US-09-848-798-110
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Matches 284; Conservative
ORGANISM: Homo sapiens
FEATURE:
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ORGANISM: Homo sapiens
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/cgn2_6/ptodata/1/ina/ea_COMB.seq:*

/cgn2_6/ptodata/1/ina/pcTUS_COMB.seq:*
                           GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
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No.
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Sequence

Sequence 358, App Sequence 206, App Sequence 201, App Sequence 215, App Sequence 215, App Sequence 217, App Sequence 13, App Sequence 13, App Sequence 113, App Sequence 114, App Sequence 114, App Sequence 114, App Sequence 117, App Sequence 312, Appl Sequence 312, Appl Sequence 312, Appl Sequence 312, Appl Sequence 117, Appl Sequence 117, Appl Sequence 117, Appl Sequence 117, Appl	TNF9
US-09-042-353-358 US-08-758-417A-206 US-09-240-274-201 US-09-240-274-211 US-09-240-274-211 US-09-240-274-217 US-09-240-274-217 US-09-378-939-13 US-08-378-939-13 US-08-378-939-23 US-08-378-939-23 US-08-053-131-184 US-08-053-131-184 US-08-053-131-184 US-08-758-417A-312 US-08-758-417A-312 US-08-758-417A-312 US-08-758-417A-312 US-08-378-939-17 US-08-259-372A-13	ALIGNMENTS 226 cus R.J.M. ibodies that Bind Human ibodies that Bind Human ibodies that Bind Human ite 510
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	RESULT SECULT SE

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Query Match 85.4%; Score 279.2; DB 4; Length Best Local Similarity 93.5%; Pred. No. 18-81; Matches 303; Conservative 0; Mismatches 18; Indels
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US-09-240-274-101
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REFERENCE/DOCKET NUMBER: BBI-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 321 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
NOLECULE TYPE: CDNA
US-09-125-098-36
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ORGANISM: Homo sapiens
FEATURE:
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241 GAAGATGTGCAACTTATTACTGTCAAAGGTATAACGCGT---CACCGTATACTTTTGGC 297
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APPLICANT: Salfeld, Jochen G.
APPLICANT: Allen, Deborah J.
APPLICANT: Allen, Deborah J.
APPLICANT: Allen, Deborah J.
APPLICANT: Raymakacalan, Sehra
APPLICANT: Kaymakacalan, Sehra
APPLICANT: Labkovsky, Boris
APPLICANT: Bankovsky, Boris
APPLICANT: Sakorafas, Brian T.
APPLICANT: Sakorafas, Paul
APPLICANT: Sakorafas, Paul
APPLICANT: Sakorafas, Paul
APPLICANT: Wilcon, Michael
APPLICANT: Wilcon, Michael
APPLICANT: Wilcon, Michael
APPLICANT: Wilcon, Michael
APPLICANT: Wilcon, Andrew J.
APPLICANT: Wilcon, Andrew J.
APPLICANT: Wilcon, Secondate Secon
STREET: 60 State Street, suite 510
CITY: Bosson
STREET: 60 State Street, Suite 510
CITY: Bassachnsetts
COUNTRY: Massachusetts
COUNTRY: USA
                                                Ouery Match
Best Local Similarity 93.5%; Pred. No. 1e-81;
Matches 303; Conservative 0; Mismatches 18; Indels 3.
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ZUD: 02109-1875
ZUD: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SURRENT APPLICATION DATA:
FILING DATE: US/09/125,098
FILING DATE:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/599,226
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: DeCont, Giulio A., Jr.
REGISTRAGION NUMBER: 31,503
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Patent No. 6258562
       US-08-599-226-36
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US-09-240-274-101

Sequence 101, Application US/09240274

Sequence 101, Application US/09240274

Patent No. 6555455

GENERAL INFORMATION:
TITLE OF INVENTION: EACH IN THEREOF

TITLE OF INVENTION: EACH IN THEREOF

TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF

TITLE OF INVENTION: US/09/240,274

CURRENT PAPLICATION NUMBER: 09/09/240,274

CURRENT PILING DATE: 1998-04-29

EARLIER PILING DATE: 1998-04.29

EARLIER PILING DATE: 1998-01-29

EARLIER PILING DATE: 1998-01-11

NUMBER OF SEQ ID NOS: 224

SOFTWARE: PARCHING VET: 2.0

SEQ ID NO 101

LENGTH: 324
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Length 321;
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**Sequence 110, Application US/09240274

**Sequence 110, Application US/09240274

**Sequence 110, Application US/09240274

**Sequence 110, Application US/0924027

**TTLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF

**TTLE OF INVENTION: UNMBER: GO/081,380

**EARLIER APPLICATION NUMBER: GO/081,380

**EARLIER PRILICATION NUMBER: GO/081,380

**EARLIER PILING DATE: 1998-04-10

**SARILER FILING DATE: 1998-04-10

**SARILER FILING DATE: 1998-10-11

**NUMBER OF SEQ ID NOS: 224

**SOFTWARE: PatentIN Ver. 2.0

**SOFTWARE: PatentIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123 AGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCTATCAAGGTT 182
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Patent No. 6255455
GENERAL INFORMATION
FORMATION
FOR APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-420.
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER APPLICATION NUMBER: 60/081,500
EARLIER FILING DATE: 1996-01-10
EARLIER FILING DATE: 1996-10-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   183 CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCGCAGCTGGCAACCTGAAGA
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Pred. No. 4.7e-76;
0; Mismatches 37;
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           303 GACCAAGCTGGAGATCAAACG 323
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88.5%;
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Best Local Similarity 88.5
Matches 284; Conservative
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US-09-240-274-210
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Sequence 112, Application US/09240274

Patent No. 625245

GENERAL INFORMATION:

APPLICANT: Siegel, Donald L.

TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL

TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF

TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF

FILE REPREBENCE: 09596-4202

CURRENT PILICATION NUMBER: US/09/240,274

CURRENT FILING DATE: 1998-04-10

EARLIER APPLICATION NUMBER: 60/081,380

EARLIER APPLICATION NUMBER: 60/081,380

EARLIER APPLICATION NUMBER: 60/081,380

SALUER PILING DATE: 1998-04-10

NUMBER OF SEQ ID NOS: 224

NUMBER OF SEQ ID NOS: 224

SEQ ID NO 112

LENGTH: 324
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88.8%; Pred. No. 1.4e-76;
iive 0; Mismatches 36;
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US-09-240-274-112
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Best Local Similarity 88.8
Matches 285; Conservative
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US-UB-37-34

Sequence 33, Application US/08378939

Patent No. 5876641

APPLICANT: CROWE, JAMES SCOTT

APPLICANT: LEWIS, ALAN PETER

TITLE OF INVENTION: PRODUCTION OF ANTIBODIES

NUMBER OF SEQUENCES: 46

CORRESPONDENCE ADDRESS:
ADDRESSE: ADDRESS:
ADDRESSE: ADDRESS:
ADDRESSE: ADDRESS:
COUNTRY: U.S.
STATE: D.C.
COUNTRY: U.S.
ZIP: 20004

COMPUTER FADABLE FORM:
MEDIUM TYPE: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BEADABLE FORM:
APPLICATION NUMBER: US/08/378,939
FILING DATE:
CLASSIFICATION ATA:
APPLICATION NUMBER: US/08/378,939
FILING DATE:
CLASSIFICATION ADATA:
APPLICATION NUMBER: US/08/378,939
FILING DATE:
CLASSIFICATION NUMBER: US/08/378,939
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               TELEFAX: (202) 783-6031
INFORMATION FOR SEQ ID NO: 31
SEQUENCE CHARACTERISTICS:
LENGTH: 324 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
                                                                                                                                                           MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRATURE:
                                                                                                                                                                                                                                                                                              NAME/KEY:
COCATION:
US-08-378-939-31
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US-08-378-939-33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 AGTICCIAAGCICCIGAICIAIGCIGCAICCACTITGCAATCAGGGGICCCAICTCGGIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 AGCCCCTAAGCTCCTGATCTATGCTGCATCCGGTTTGCAAGTGGGGTCCCATCAAGTT
                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                            Query Match

80.1%; Score 261.8; DB 4; Length 324;
Best Local Similarity 88.5%; Pred. No. 4.7e-76;
Matches 284; Conservative 0; Mismatches 37; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 7

US-08-378-939-31

US-08-378-939-31

Sequence 31, Application US/08378939

Patent No. 5876561

APPLICANT: CROWE
TITLE OF INVENTION: PRODUCTION OF ANTIBODIES

NUMBER OF SEQUENCES: 46

CORRESPONDENCE ADDRESS:

CORRESPONDENCE ADDRESS:

ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
STATE: D.C.

COUNTRY: 0.5.

STATE: D.C.

COUNTRY: N. W.

STATE: D.C.

COUNTRY: D.C.

COUNTRY: BADABLE FORM:

MEDIUM TYPE: Floppy disk

COUNTRY: READABLE FORM:

MEDIUM TYPE: Floppy disk

COUNTRY: PE: Floppy disk

COUNTRY: BADABLE FORM:

MEDIUM TYPE: Floppy disk

COUNTRY: BADABLE FORM:

MEDIUM TYPE: GONDELIDE

SOFTWARE: PatentIn Release #1.0, Version #1.25

RIGH APPLICATION UNDBER: US/08/378,939

FILING DATE: 01.DEC-1992

ATTORNEY, AGENT INFORMATION:

REFERENCE/DOCKET NUMBER: US 07/952640

REFERENCE/DOCKET NUMBER: 1888-118

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
                                                                          LENGTH: 324

TYPE: DNA

ORGANISH: Homo sapiens

FEATURE:

OTHER INFORMATION: anti-Rh(D) antibody clone SH34
US-09-240-274-210
NUMBER OF SEQ ID NOS: 224
SOFTWARE: Patentin Ver. 2.
SEQ ID NO.210
LENGTH: 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           246
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240

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US-09-240-274-220
                                                                                         ; OTHER INFORM
US-09-343-485A-3
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SEQ ID NO 220
LENGTH: 324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAAAGGTGCCCCTCCGAGTACGTTCGGC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 GAAGATTTTGCAACTTATTACTGTCAACAGGATAACAGT---TATCCTTTCACTTTCGGC 297
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Facent No. 641377
Facent No. 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GACATTCAGCTGACCCAGTCTCCATCCTCCTGTCTGCATCTGGGGGGGACACAGTCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 ATCACTIGICGGGCAAGICAGGGCATTAGCAATAATTTAGCCIGGTATCAGCAGAAACCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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Best Local Similarity 89.6%; Pred. No. 1.3e-75;
Matches 292; Conservative 0; Mismatches 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACT
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                                                                               1808-118
                                                                                                                                                               TELEFAX: (202) 783-6031
TELEFAX: (202) 783-6031
SEQUENCE CHARACTERISTICS:
LENGTH: 324 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
NAME FERNST, BARBARA G
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 18
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 783-6040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
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SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: CDNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE: NO FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 19040
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US-08-378-939-33
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                                                                                                                                                                                                                                                                                                                                                                                                    121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Siegel, Donald L.
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RA!(D) - BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-42U2
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
BARLIER FILING DATE: 1999-04-10
EARLIER FILING DATE: 1998-04-10
BARLIER FILING DATE: 1998-04-10
BARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62
                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GACATCCAGATGACCCAGTCTCCATCCTCCTGTCTGCATCTGTAGGAGACAGAGTCACC
                                                                                                                                                                                                                                                                                                     61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 CGAGCTCACACAGTCTCCATCCTTCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC
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Description of Artificial Sequence: Synthetic DNA referred to as "Mandy"
                                                                                                                                                    3;
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                                                                                                   Length 19040;
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                                                                                                                                                    Indels
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                                                                                                      DB 4;
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Pred. No. 5.1e-75;
0; Mismatches 39;
                                                                                                                                                    32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: anti-Rh(D) antibody clone SH51
US-09-240-274-220
                                                                                                   Score 259.8; DB 4
Pred. No. 9.6e-75;
0; Mismatches 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7908 CAAGGGACCAAGGTGGAAATCAAACGT 7934
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Patent No. 6255455
                                                                                                   79.4%;
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87.9%;
                                                                                                 Query Match
Best Local Similarity 89.33
Matches 292; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 87.9°
Matches 282; Conservative
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ORGANISM: Homo sapiens
       OTHER INFORMATION: OTHER INFORMATION:
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; TYPE: DNA
ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I02
US-09-240-274-102
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US-09-240-224
Sequence 224, Application US/09240274
Farent No. 6255455
Farent No. 6255455
FARENT NO. 6255455
FARENT NO. 6255455
FILE REPERENCE: 05596-4202
FILE REPERENCE: 05596-4202
FURRENT APPLICATION NUMBER: US/09/240,274
FARLIER APPLICATION NUMBER: US/09/240,274
FARLIER APPLICATION NUMBER: 06/081,380
FARLIER APPLICATION NUMBER: 60/081,380
FARLIER APPLICATION NUMBER: 60/081,380
FARLIER APPLICATION NUMBER: 60/081,380
FARLIER FILING DATE: 1998-01-0
FARLIER FILING DATE: 1998-01-0
FARLIER FILING DATE: 1996-10-11
FARLIER FILING DATE: 1996-10-11
FARLIER FILING DATE: 1996-10-11
FARLIER FILING DATE: 1996-10-11
FARLIER PLING DATE: 1996-10-11
FARLIER PLING DATE: 1996-10-11
                           CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGGAGGA 245
123 AGCCCCTAAGCTCCTAATCTATGCTGCATCCACTTTGCAAAGTGGGGGTCCCATCAAGGTT 182
                                                  66 TTGCCGGGGGAGTCAGGGCATTAGCAATTTTAGCCTGGTATCAGCAGAAACCAGGGAA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 AGTTÇÇTAAGÇTÇÇTGATÇTATGÇTGÇATÇÇAÇTTTGÇAATCAGGGGTÇÇÇATÇTÇGGTT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                186 cAGTGGCAGTGGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGA 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               243 TTTTGCAACTTACTGCTGTCAACAGGGTTACAGTACCCTCCGTACAGTTTTGGCCAGGG 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 79.1%; Score 258.6; DB 4; Length Best Local Similarity 87.9%; Pred. No. 5.1e-75; Matches 282; Conservative 0; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
ORGANICAM: Homo sapiens
; FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH56
                                                                                                                                        306 GAÇÇAAGGTGGAAATÇAAAÇG 326
                                                                                                                                                                303 GACCAAAGTGGATATCAAACG 323
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US-09-240-274-218
// Sequence 218, Application US/09240274
// Sequence 218, Application US/09240274
// Sequence 218, Application US/09240274
// Patent No. 6255455
// GENERAL INFORMATION: Donald L.
// TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
// TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
// TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
// FILE REFERENCE: 09596-4202
// CURRENT FAPLICATION WUMBER: US/09/240,274
// CURRENT FILING DATE: 1998-01-29
// SARLIER APPLICATION WUMBER: 60/081,380
// BARLIER APPLICATION WUMBER: 60/028,550
// BARLIER FILING DATE: 1996-10-11
// WUMBER OF SEQ ID NOS: 224
// SOFTWARE: PatentIN Ver. 2.0
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF FILE REFERENCE: 05596-4202
CURRENT APPLICATION NUMBER: US/99/240,274
CURRENT PILLING DATE: 1999-01-29
FEARLIER APPLICATION NUMBER: 60/081,380
FEARLIER PILLING DATE: 1998-04-10
FEARLIER FILING DATE: 1998-04-10
FEARLIER FILING DATE: 1998-04-10
NUMBER OF SEQ ID NOS: 224
SOCTHARE: PATENTIN OF SEQ ID NOS: 224
SEQ ID NO 102
LENGTH: 321
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ORGANISM: Homo sapiens
PEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH49
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PatentIn Ver. 2.0
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SEQ ID NO 222
LENGTH: 321
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FACENTE NO. 0.273455

FITLE NO. 0.273455

FITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF

FILE REFERENCE: 09596-4202

FILE REFERENCE: 09596-4202

FILE REFERENCE: 09596-4202

FILE REPLICATION NUMBER: 05/09/240,274

CURRENT APPLICATION NUMBER: 60/081,380

EARLIER APPLICATION NUMBER: 60/01,380

EARLIER FILING DATE: 1998-04-10

EARLIER FILING DATE: 1996-10-11

NUMBER OF SEQ ID NOS: 224

SOFTWARE: PACENTIN VET: 2.0

SEQ ID NO 221

LENGTH: 321
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78.6%; Score 257; DB 4; Length 321;
Best Local Similarity 89.7%; Pred. No. 1.7e-74;
Matches 288; Conservative 0; Mismatches 30; Indels
                                                                       Length 321;
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US-09-240-274-221
                                                                   Score 257; DB 4;
Pred. No. 1.7e-74;
0; Mismatches 30
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18-09-240-274-221
Sequence 221, Application US/09240274
Patent No. 6255455
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Matches 288; Conservative
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US-09-240-274-218
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APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RA(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-42U2
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
BARLIER FILING DATE: 1998-04-10
EARLIER FILING DATE: 1998-04-10
BARLIER FILING DATE: 1998-04-10
BARLIER FILING DATE: 1998-04-10
BARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
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Job time : 18.3396 secs
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ENTS ENTS p Dibody line) rity de g varie	Craniata, Vertebrata, Catarrhini, Hominidae,
DB ID HSVK4H2FG E E01736 E E01737 9 HSUK4H2FG E E01737 9 HSUB6791 9 HSUB6791 9 HSUB6791 9 HSUB6791 9 HSUB6791 9 AR08878 E E05868 9 HUMIGLCDR 9 AR08878 6 AR08878 6 AR08878 9 AR455557 9 HSVKAP4 9 AR064111 6 I12039 A AB064111 6 I12039 A AB064080 A AB064111 6 I12039 A AB064080 A AB064080 A AB064080 A AB064080 A AB064080 A AS130034 A AS121 A AR096963 A AS2534 A AR096963 B HSUB114L A AR096963 B HSUBUD14L A AR096964 A AR096964 B HSUBARURS B E05213 B AR103492 B HSUBARURS C E0523 A AR096964 A AR096964 B AR096964 A AR096964 A RO99195 S 71450 ALIGNMENTS ALIGNMENTS ALIGNMENTS 1 Complementarity determining ign variable region yetemic lupus erythematosus.	ordata; imates;
	Eutheria; 1 to 339)
Ouery Query Query Auch Length D 339 100.0 339 100.0 339 100.0 339 100.0 339 100.0 339 100.0 339 100.0 339 100.0 339 100.0	Homo sapiens Homo sapiens Eukaryota; Me Mammalia; Eut 1 (bases 1 t
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Nakatani,T., Nomura,N., Horigome,K. and Noguchi,H.
MUMAN ANTIBODY. ANTIBODY GENE AND CORRESPONDING RECOMBINANT Patent: JP 1988267295-A 5 04-NOV-1988; SUMITOMO CHEM CO LTD, SUMITOMO PHARMACEUT CO LTD
Manheimer-Lory, A., Katz, J.B., Pillinger, M., Ghossein, C., Smith, A. and Diamond, B.
Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype
J. Exp. Med. 174 (6), 1639-1652 (1991)
1660528
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/iorganism="Homo sapiens"
/iorganism="Buttern HER(SLE)"
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/iore="Igg light chain variable region"
/io. 120
/iore="complementarity determining region, CDR 1"
/iore="complementarity determining region, CDR 284. 284. 284. 282 g 75 t
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Best Local Similarity 100.0%; Pred. No. 3.3e-100;
Matches 339; Conservative 0; Mismatches 0; Indels
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PN - JP 1988267295-A/5
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PD 04-NOV-1988
PF 26-NOV-1988
PP 26-NOV-1987 JP 1987298513
PR 03-DEC-1986 JP 86P 288340
PI NAKATANI TOMOSUKE, NOMURA NORIKO, HORIGOME KAZUHIKO, PI
NOGUCHI HIROSHI
PC C12P21/02,C07H21/04,C07K13/00,C07K15/12,C12N15/00,(C12P21/02,
PC (12P21/02,C12H1:91);
PC (12P21/02,C12H1:91);
CC (12P21/02,C12H1:91);
CC strandedness: Double;
CC topology: Linear;
CC topology: Linear;
CC hypothetical: No;
CC hypothetical: No;
CC hypothetical: No;
FH Key
FT sig_peptide 1. .60
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1 (Dases 1 to 619)
Nakatani,T., Nomura,N., Horigome,K. and Noguchi,H.
Nakatani,T., Nomura,N., Horigome,K. and Noguchi,H.
Patent: JP 198826725ANTIBODY GRESPONDING RECOMBINANT Patent: JP 198826725AA 4 04-NOW-1988; SUMITOMO CHEM CO LID, SUMITOMO PHARMACEUT CO LID
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/product='mature peptide of V region
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_110 c 100 g 97
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61 ATCAACTGCAAGTCCAGGCGAGGTGTTTATACAGCTCCAACAATAAGAACTACTTAGCT 120
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      HUMAN ANTIBODY, ANTIBODY GENE AND CORRESPONDING RECOMBINANT PATENT: JP 1988267295-A 6 04-NOV-1988; SUMITOMO CHEM CO LID, SUMITOMO PHARMACEUT CO LID
                                                                                                     26-NOV-1987 JP 1987298513
03-DEC-1986 JP 86P 288340
NAKATANI TOMOSUKE, NOMURA NORIKO, HORIGOME KAZUHIKO,
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Pred. No. 5.4e-96;
0; Mismatches 8;
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96 c 83 g 76
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                                                                                                                                                                                                                      strandedness: Double;
topology: Linear;
hypothetical: No;
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                                                                    JP 1988267295-A/6
04-NOV-1988
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ilarity 97.6%;
Conservative
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PD 04-NOV-1988
PF 03-DEC-1986
PR 03-DEC-1986
NOGUCHI HIROSHI
PC C12R21/02,C0
PC C12R21:19),
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:9606"
_138 c 135 g 169
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(C12P21/00,C12R1:91);
strandedness: Double;
topology: Linear;
hypothetical: No;
anti-sense: No;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Sasse 1 to 355)
Pritsch,O., Troussard,X., Davi,F., Macro,M., Dumas,G., Magnac,C.,
Clerget,F., Schroeder,H.W., Leporrier,M. and Dighiero,G.
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/protein id="AAB48604.1"
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L11700

V.region; complementarity determining region; immunoglobulin light chain; monoclonal antibody.

Homo sapiens CDNA to mRNA.
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Pritsch, O., Troussard, X., Davi, F., Macro, M., Dumas, G., Magn

Clerget, F., Schoeder, H.W., Leporrier, M. and Dighiero, G.

Direct Submission

Submitted (24-JAN-1997) Unite d'Immunohematologie et

d'Immunopathologie, Institut Pasteur, 28, rue du Dr. Roux,

75724
Restricted VH clan usage by siblings affected with Chronic Lymphocytic Leukemia
Unpublished
                                                                                                                                                                                                                          /map="2p11-2"
/cell type="B cells"
/note="patient with Chronic Lymphocytic Leukemia"
1. 355
/gene="CLL-L1B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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Best Local Similarity 97.6%; Score 326.2; DB 9; Length 355;
Best Local Similarity 97.6%; Pred. No. 5.4e-96;
Matches 331; Conservative 0; Mismatches 8; Indels 0
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1. .355
/organism="Homo sapiens"
/db_xxef="taxon:9606"
/chromosome="2"
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/gene="CLL-L1B"
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121 TGGTACCAGAAAACCAGAAACAGCTCCTAAACTGGTCATTTACTGGGCATCTACCCGG 180
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteeleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 372) Hoon, D.S., Wang, Y., Sze, L., Kanda, H., Watanabe, T., Morrison, S.L., Morton, D.L. and Irie, R.F. Molecular cloning of a human monoclonal antibody reactive to ganglioside GM3 antigen on human cancers 63 (21), 5244-5250 (1993) 94036806
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/db xref="taxon:9606"
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/tissue_type="blood"
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Hosokawa,S., Tagawa,T., Hirakawa,Y., Ito,N. and Nagaike,K.
Human monoclonal antibody specifically binding to surface of cancer. Beatent: US 5990287-A 4 23-NOV-1999;
Location/Qualifiers
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Pred. No. 2e-94;
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96.8%;
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Mariette, X.

Direct Submission
Submitted (29-OCT-1992) Xavier Mariette, Laboratoire d'
Submitted (29-OCT-1992) Xavier Mariette, Laboratoire d'
Immunopathologie, Hopital, Saint-Louis, 1, avenue Claude Vellefaux,
Paris, 75010, France
Location/Qualifiers
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Patent: US 5837845-A 4 17-NOV-1998;
Location/Qualifiers
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                                                                                              /organism="Homo sapiens"
/db xref="taxon:9606"
/ceIl_line="Epstein-Barr transformed lymphoblastoid
|line"
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Sequence 4 from patent US 5837845.
AR058974
AR058974.1 GI:5984551
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1. 339
/product="kappa chain"
/note="VK IV family"
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RESULT 10 AR088878

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HUMIGKAW 11near PRI 04-JAN-1995 MRNA linear PRI 04-JAN-1995 Muman Ig rearranged kappa-chain mRNA V-J1-region, hybridoma AE6-5, end.
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J-region, V-region; immunoglobulin-kappa; processed gene; variable
region subgroup VK.IV.
Human (patient POP) hybridoma AE6-5 DNA, clone pHuUCVK, derived
Homo sapiens
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Spatz,L.A., Wong,K.K., Williams,M., Desai,R., Golier,J., Cleman,J.E., Alf.F.W. and Latov,M. Cloning and sequence analysis of the VH and VL regions of an anti-myelin/DNA antibody from a patient with peripheral neuropathy Immunol: Jymphocytic leukemia (1990)
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28-JUN-1991 JP 91P 158861
PI HOSOKAWA SIRIKO, TAGAWA TOSHIAKI, HIRAKAWA YOKO, ITO NORIHIKO, PI HOSOKAWA SIRIKO, TAGAWA TOSHIAKI, HIRAKAWA YOKO, ITO NORIHIKO, PI NAGAIKE KAZUHIRO
PC (12P21/08,A61K39/395,C12N5/28,C12N15/13//A61B10/00,C12N15/08,QPC (212P21/08,C12R1:91);
PC (12P21/08,C12R1:91);
CC strandedness: Single;
CC strandedness: Single;
CC topology: Linear;
CC topology: Linear;
CC topology: Linear;
CC Location/Qualifiers
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Location/Qualifiers
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/organism="synthetic construct"
/db_xref="taxon:32630"
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E05868.1 GI:2174055
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HUMAN TYPE MONOCLONAL ANTIBODY AND GENE CODING THE SAME, HYBRIDOMA AND ANTITHORN AGENT
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AND SHITTENBISH KASEI CORP
PN JP 1993304987-A 4 19-NOV-1993;
MITSUBISH KASEI CORP
PN JP 1993304987-A/4
PP 22-JUN-1992 JP 1992162849
PR * 28-JUN-1991 JP 91P 158859, 28-JUN-1991 JP 91P 158860, PR
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                                                                                                                                                                                                                                                     Unknown.
Unclassitied.
1 (bases 1 to 342)
Hosokawa,S., Tagawa,T., Hirakawa,Y., Ito,N. and Nagaike,K.
Human monoclonal antibody specifically binding to surface of cancer cell membrane
Patent: US 5990297-A 4 23-NOV-1999;
Location/Qualifiers
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0
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  CCGTGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
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                                                                                                              342 bp
Sequence 4 from patent US 5990297.
AR088878
AR088878.1 GI:10015639
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92 c 87 g
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61 61 121 121 181

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source BASE COUNT ORIGIN

JOURNAL

FEATURES

241

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301 301

ò g LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS

RESULT 11 E05868

SOURCE ORGANISM

REFERENCE AUTHORS TITLE

JOURNAL

COMMENT

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/translation="MVLQTQVFISLLIWISGAYGDIVMTQSPDSLAVSLGERATINCK SSQSLLYSSNNKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGTDFTLTIS SLQAEDVAVYYCQQYXSTPPMFGQGTKVEIKRTVAAPSV"

124 c 120 g 109 t
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HOMO Sapiens, Similar to immunoglobulin kappa constant, clone
MCG:22669 IMAGE:4274551, mRNA, complete cds.
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Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Strausberg,R.
Direct Submission
Submitted (03-DEC-2001) National Institutes of Health, Mammalian
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                /codon_start=1
/product=1immunoglobulin M light chain V region"
/protein id="AAB24404.1"
/db_xref="G1:261240"
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                                                                                                                                                                                            gene="immunoglobulin M light chain V region"
88 .460
'Partial
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Pred. No. 2.1e-94;
0; Mismatches 11; Indels 0;
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/note="anti-lipid A antibody; This sequence
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/organism="Homo sapiens"
/db_xref="taxon:9606"
1. .460
/partial
 Hybridoma 11 (5), 667-675 (1992)
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96.8%;
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SSQSLLYSSNNKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS
SLQAEDVAVYXCQQYXSTPPMFGQGTKVEIKRT"
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(Dases 1 to 460)

Dorai, H., Bubbers, J.E. and Gillies, S.D.

Cloning and reexpression of a functional human IgM anti-lipid A antibody
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/gene="IGKV"
/note="Ig kappa-chain V-J1-region precursor"
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llarity 96.8%; Pred. No. 2.1e-94;
Conservative 0; Mismatches 11;
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Homo sapiens
                                                                                                                                                                     /proteIn_id="AAA58916.1"
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1. 405
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                                                                                                                                                                                                                                                                                                                                                               /product="Ig kappa-chain"
369. .370
/gene="IGKV"
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110 c 101 g 99
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us-09-627-896b-26.rge

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completed: July 18, 2003, 13:47:35 e: 949.849 secs
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Best Local Similarity 96.5%;
Matches 327; Conservative (
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                                                                                     Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONTECH
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M.; Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
R. M.
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ACEVTHQGLSSPVTKSFNRGEC"
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                                                                                                                                                                                                                                                                                   Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 35 Row: i Column: 15 This clone was selected for full length sequencing because it passed the following selection criteria: GenomeScan gene prediction, Similarity but not identity to protein.
  3ene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2599,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
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                                                    NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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Homo sapiens clone RIZMVL6 anti-cardiolipin immunoglobulin light
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by.P., Soley.A., Cerutti,M., Freyssinet,J.M., Pasquali,J.L. and
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                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (05-DEC-2001) Laboratoire d'immunopathologie, Institut
d'Immunologie et d'Hematologie, 1 place de l'Hopital, Strasbourg
67091, France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG
                                                                                                                                                                                                                                                                 Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostor
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 342)
Lieby, P., Soley, A., Cerutti, M., Freyssinet, J.M., Pasquali, J.L.
Martin, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GACATCGTGATGACCCCAGTCTCCCTGGCTCTGTCTCTGGGCCGAGAGGGCCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT
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Pred. No. 6.9e-94;
0; Mismatches 12;
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Primates;
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BM768906 K-EST0051
BG370753 602438602
BQ707260 AGENCOURT
BG534966 602554155
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BM78342 K ESTU061
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AW406484 UI-HF-BL0
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BG398034 602439564
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                                GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
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K-EST0105 602568157

EST363649 601811013

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AW405821 641 bp mRNA linear EST 16-FEB-2000 UI-HF-BLO-abp-h-07-0-UI.rl NIH MGC_37 Homo sapiens cDNA clone IMAGE:3057636 5', mRNA sequence.
AW405821 GI:6924878
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Homo sapiens

Mammalia; Mutheria; Primates; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Missis 1 to 641)

Mational Institutes of Health, Mammalian Gene Collection (MGC)

Mational Institutes of Health, Mammalian Gene Collection (MGC)

Morbolished (1999)

Contact: Robert Strauberg, Ph.D.

Email: Capubs-romail.nih.gov

Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDM Library Preparation: M.B. Soares Lab

CDM Library Arrayed by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab
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ilarity 96.8%; Pred. No. 2.1e
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Eutheria; Butheria; Primates; Catarrhini; Hominidae; Homo.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 886)
S NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: Gapbs-ramail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
CONA Library Preparation: CLONETECH Laboratories, Inc.
CONA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CONA Library Arrayed by: Incyte Genomics, Inc.
CONA Library Arrayed by: Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLCM1091 row: p column: 08
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BF674779.1 GI:11948674
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Sao Paulo-SP,

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/ Organism="Homo sapiens"
/ Organism="Homo sapiens"
/ dbx racf="taxon:9606"
/ clone_lib="UM0071"
/ dev stage="Adult"
/ dev stage="Adult"
/ note="Organ: uterus; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from CRESTES PCR (U.S. Letters Patent application No. 196
/ 716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low
stringency conditions."
                                                                                                                               Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=IL5-UM0071-120 400-065-d06&t3=2000-04-12&t4=1)
Seq primer: puc 18 forward
High quality sequence stops: 419.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 915)
NIH-MGC http://mgc.nci.nih.gov/.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 318.2; DB 10; Length 533;
Pred. No. 1.7e-86;
      Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCCTCACTTTCGGCGGAGGGACCAAGGTGGAGATCAAA 353
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                                                                                                                                                                                                                                                                                                   /note="Vector: pT7T3-Pac, Site 1: Not1; Site 2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
Constructed from size fractionated cytoplasmic mRNA
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 53)

1 (bases 1 to 53)

1 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AW802126 533 bp mRNA linear EST 16-MAY-2000 ILS-UM0071-120400-065-d06 UM0071 Homo sapiens cDNA, mRNA sequence.
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 319.8; DB 10;
Pred. No. 5.9e-87;
                                                                                                                                                                                            /clone lib="NIH MGC 37"
/tissue_type="lymph"
/cell_type="germinal center lycell_line="MGC8"
/lab_host="DH10B (LTI)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                      /organism="Homo sapiens"
                                                                                                                                                     /db_xref="taxon:9606"
/clone="IMAGB:3057636"
                                                                                           Location/Qualifiers
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al Similarity 96.5%;
327; Conservative
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9 74

Gaps

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13; Indels

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RS HCGP http://www.ludwig.org.br/ORESTES.
The PAPESP/LICR Human Cancer Genome Project
The PAPESP/LICR Human Cancer Genome Project
Contract: Simpson A.J.G.
Ludwig Institute for Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the PAPESP/LICR Human Cancer Genome
(http://www.ludwig.org.br/scripts/gethtml2:pl?tl=CM2&t2=CM2-ST0182-
Sag ptimmer: puc 18 forward
High quality sequence start: 7
Location/Qualifiers
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| / organism="Homo sapiens" |
| / organism="Homo sapiens" |
| / db xref="raxon:9606" |
| / dcv=stage="Adult" |
| dcv=stage="Adult"
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91.5%; Score 310.2; DB 10; Length
Best Local Similarity 94.7%; Pred. No. 5.1e-84;
Matches 321; Conservative 0; Mismatches 18; Indels
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AL Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be http://image.llnl.gov
Plate: LLCML283 row: o column: 16
High quality sequence stop: 764.
Iloration/Qualifiers

Location/Qualifiers

/ Ab Location/Qualifiers

/ Ab Location/Qualifiers

/ Ab Dost = "MAGE: 465591"
/ Clone = "IMAGE: 456591"
/ Clone = "IMAGE: 456591"
/ Clone = "IMAGE: 456591"
/ Lissue Lype="Type" primary B-cells from tonsils (cell line)"
/ Ab Dost = "DH100 (phage-resistant)"
/ Ab Dost = "Constructed by ling following 5' adaptor: GGCAGCGG(G) Size-selected should be extended by using following 5' adaptor: GGCAGCGG(G) Size-selected should be extended by using following 5' adaptor: GGCAGCGG(G) Size-selected should be extended by using California Berkeley) using ZaP-caDNA synthesis kit california size and Superseript II RT (Life Technologies).

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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleo
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                          NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
                                                                                                                                         (bases 1 to 508)
                                                                                                                                                                                                      Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db xref="taxon:9606"
/dlone="IMAGE:4054205"
/clone="IMAGE:4054205"
/clone="IMAGE:4054205"
/clone="IMIH MGG 48"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="MDH108 (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site_1: Xho1;
Site_2: EcoR1; cDNA made by oligo-dT priming.
Directionally cloned into EcoR1/Xho1 sites using the following 5 adaptor: GGCACGAGG(G). Size-selected >SObpp for average insert eize 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of Callfornia, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH MGC Library."
2 others
                                                                 E (Dases 1 to 691)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Lunpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM994 row: c column: 06
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Pred. No. 5.2e-84;
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96.8%; Pred. No. 5...
0; Mismatches
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Matches 328; Conservative
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Email: cgapbs-remail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.
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AW404610
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DEFINITION
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UI-W-)/2 508 bp mRNA linear EST 16-FEB-2000 UI-W-)/2 COUL.x1 NIH MGC_37 Homo sapiens cDNA clone AW406572

DEFINITION

AW406572

ACCESSION

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1...904

(Organism="Homo sapiens"

(Ab_xref="taxon:8606"

(Clone="InAd8:6278306"

(Clone="InAd8:6278306"

(Clone="Lib="NIH MGC 113"

(Iab host="Hollo (phage-resistant)"

Into Bcorgan: spleen; Vector: pOTB7; Site 1: XhoI; Site 2: EcoR1; CDNA made by oligo-dT priming. Directionally cloned and the Bcorgan; Spleed; Vector: potB7; Site 1: XhoI; Site 2: Into EcoR1/XhoI sites using the following 5' adaptor: Into Bcorgan, Mande by oligo-dT priming. Directionally cloned GGCACACAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Superscript II R. Life Technologies). Note: this is a 264 c 219 g 212 t lothers
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Best Local Similarity 93.8%; Score 305.4; DB 14; Length 904;
Matches 318; Conservative 0; Mismatches 21; Indels 0;
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                                                                                                           Homo sapiens

Bukaryote; Mecazoa; Chordata; Craniata; Vertebrata; Euteleostom; Eukaryote; Mecazoa; Chordata; Catarrhini; Hominidae; Homo.

Bukaryote; Mecaron: nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Eco RI site shown at the beginning of the sequence.

Contact: Robert Strausberg, M.B. Soares Lab

Contact: Robert Strausberg, M.B. Soares Lab

Contact Strauspergoration: M.B. Soares Lab

Contact Strauspergoration: M.B. Soares Lab

Contact Day, M.B. Soares Lab

Contact Strauspergoration: M.C. Clone distribution: MGC Clone distribution information can be conditioned through the I.M.A.G.E. Consortium/LINL at:

Seq primer: M13 Forward.

Location/Qualifiers

| Consortion/Qualifiers | Consortium/LINL at:
| Clone | Liberaron:9666" | Consortium/CMBC 37" | |
| Colone | Liberaron:9666" | Colone | Liberaron:9666" |
| Consortium/CMBC 30 | Colone | Liberaron:9666" |
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Best Local Similarity 93.8%; Pred. No. 1.4e-82;
Matches 318; Conservative 0; Mismatches 21; Indels 0; Gaps
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AW404610.1 GI:6923667
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                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 630)
                                                                                                                                                                                                                                                                                                                                                                                                              Contract: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Eco II site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
Clone distribution: M.G. Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GACATCCAGTTGACCCCAGTCTCCCTGGCTGTGTCTCTGGGCGAGAGGCCCACC
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                UI-HF-BL0-acu-a-09-0-UI.rl NIH MGC_37 Homo sapiens cDNA clone IMAGE:3060017 5', mRNA sequence.
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|db_xref="taxon:9606"
|clone="IMAGE:3060017"
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                                                                                AW406512
AW406512.1 GI:6925569
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RESULT 12 BG426036

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BG426036 798 bp mRNA linear EST 14-MAR-2001
602492715F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4606658 5',
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11H-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                  Conteact: Robert Strausberg, Ph.D.
Email: Ggapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1345 row: n column: 03
High quality sequence stop: 542.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .798
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                                                                                              BG426036.1 GI:13332542
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Best Local Similarity 93.5%;
Matches 317; Conservative 0
                                                   mRNA sequence.
                                                                                                                                                                         Homo sapiens
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Tel: +55-11-2704922
Fax: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome (http://www.ludwig.org.br/carcipes/gethtml2.pl?tl=IL3&t2=IL3-ET0116-28400-10-28&t4=1)
Seq primer: puc 18 forward = 10-28&t4=1)
High quality sequence start: 46
High quality sequence start: 46
High quality sequence starp: 99.
Location/Qualifiers

// Organism="Homo sapiens"
// Organism="Homo thing-tunor; Vector: puc18; Site 1: Smal; Anvients Inng-tunor; Vector: puc18; Site 1: Smal; Site 2: Smal; A mini-library was made by cloning products
// Ordanism="Homo thing-tunor; Vector: puc18; Site 1: Smal; Site 2: Smal; A mini-library was made by cloning products
// Ordanism="Homo thing-tunor; Vector: puc18; Site 1: Smal; Site 2: Smal; A mini-library was made by cloning products
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// Ordanism="Homo thing-tunor; Vector: puc18; Site 1: Smal; Site 1: Smal; Site 2: Smal; A mini-library was made by cloning products
// Ordanism="Homo thing-tunor; Vector: puc18; Site 1: Smal; Site 
                                                                                                                                                                                                                                       1L3-E-0116-281000-308-H01 ET0116 Homo sapiens CDNA, mRNA sequence.
BF870122.1 GI:12260252
BST.
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
I (bases 1 to 53)
Dias Neto, E., Garcia Correa, K., Verjovski-Almeida, S., Briones, M.R., Godian, G.H., Carvalho, A.F., Matsukuma, A., Baidi, S., Sinya, M.B., Brunstein, A., Geoliveira, P., Matsukuma, A., Baia, G.S., Simpson, D.H., M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Singson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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89.1%; Score 302.2; DB 12; Length 553;
Best Local Similarity 93.2%; Pred. No. 1.3e-81;
Matches 316; Conservative 0; Mismatches 23; Indels 0;
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/db.xef="Laxon:666"
/dlone="InMAGE:471666"
/dlone="InMAGE:4716948"
/dlone=lib="NIH MGC 77"
/lote="Organ: lung' Vector: pDNN-LIB (Clontech); Site 1: Sfil (ggocgetcaggoc); Site 2: Sfil (ggocgetcaggoc); Site 2: Sfil (ggocgetcataggoc); Site 2: Sfil (ggocgetcaggoc); Site 2: Sfil (ggocgetcaggoc); Site 2: Sfil (ggocgetcataggoc); Site 2: Sfil (ggocgetcaggoc); Site 2: Sfil (ggo
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Eukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi;
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi;
Eukaryota, Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Danalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Some of the standary of Health, Mammalian Gene Collection (MGC)

(Contact: Robert Strausberg, Ph.D.

(Contact: Robert Strausberg, Ph.D.D.

(Contact: Robert Strausberg, Ph.D.

(Contact: Robert Strausbe
                                                                                    BG55993
602590249FI NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4716948 5',
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Best Local Similarity 95.0%; Pred. No. 1.4e-81;
Matches 323; Conservative 0; Mismatches 16; Indels 1;
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181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGGGGTCTGGGACAGATTTCACTCTCACC 240
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                                                                             ATCAGCAGCCTGCAGGCTGAAGATGTGGCCAGTTTATTACTGTCAGCAATATTATAGTACT 300
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S. NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

Dational Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: gapbs-rammali.nih.gov

Tissue Procurement: CLONTECH Laboratories, Inc.

CDNA Library Prrayed by: The I.M.A.G.E. Consortium (Link)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Link at:

http://image.lini.gov

Plate: LLCM1376 row: b column: 19
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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BG484518.1 GI:13416797
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0; Mismatches 11; Indels
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Location/Qualifiers
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Best Local Similarity 95.0
Matches 322; Conservative
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Noguchi H;

Nakatani T, Nomura N, Horigome K,

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| SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
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                                                                                                                                                               1 gacatccagttgacccagtc......ggaccaaggtggaaatcaaa 339
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| SIDS2/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
| SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
| SIDS2/gcgdata/geneseq/geneseqn-embl/NA201B.DAT:*
| SIDS2/gcgdata/geneseq/geneseqn-embl/NA201B.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                  /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*/SIDS2/gcgdata/geneseq/
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Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                             2185239 seqs, 1125999159 residues
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Listing first 45 summaries
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AAN80498
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                                                             nucleic search, using sw model
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339
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(SUMO ) SUMITOMO CHEM IND KK.
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                                                                                                                                                                 Gaps
                          New gene encoding for antibody to Pseudomonas aeruginosa exotoxin plus recombinant vectors and host cells, useful for treating infections.
                                                                               Sequence encodes variable region of light chain of anti-exotoxin antibody. It encodes the same protein sequence as AAN80498 except that the signal sequence of AAN80498 contains an intron. See also AAN80495-N80496, AAN80498 and AAN80911-2.
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                                                                                                                                               DB 9; Length 400;
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96.7%; Score 327.8; DB 9; Length
Best Local Similarity 97.9%; Pred. No. 2.4e-95;
Matches 332; Conservative 0; Mismatches 7; Indels
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lambda gFK1; ss.
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                                                                                                                             Seguence 400 BP; 93 A; 109 C; 101 G; 97 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        region of FK-001 from lambda gFK1.
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532..882
/*tag= a
/product=V region
                                                              Claim 5; page 27; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                  AAN80941 standard; DNA; 1373 BP
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WPI; 1988-156310/23.
P-PSDB; AAP80894.
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26-NOV-1987;
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                                                                                                                                                                                                                                                                                                                                            Genomic DNA was isolated from the Epstein Barr virus-transformed human cell line FK001, fragmented and a gene library constructed. The library was screened with H or L chain probes and positive clones were identified including lambda gFK1. This clone contained an 11.5kb insert encoding the V and C regions of Kappa chain. Ecost digested vector pSV2neo was end-filled and then blunt-end ligated to a Sall linker to form pSV2neoSall. This plasmid and pSV2neoGFK1 which was itself digested with Sall and ligated together to form pSV2neoGFK1 which was itself digested with Pvul The plasmid pSV2neoGFK1 which was itself digested with Pvul and a mixture of the two was used to transform mouse myeloma cells which then expressed the antibody.
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                                                                                                                       New gene encoding for antibody to Pseudomonas aeruginosa exotoxin plus recombinant vectors and host cells, useful for treating infections.
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96.7%; Score 327.8; DB 9; Length 1373;
Bast Local Similarity 97.9%; Pred. No. 46-95;
Matches 332; Conservative 0; Mismatches 7; Indels 0;
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Noguchi H;
Horigome K,
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    Nomura N,
                                                                     WPI; 1988-156310/23
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                                                                                                                                                                                                                                                         Sequence encodes variable region of light chain of anti-exotoxin antibody. The signal sequence contains an intron which is spliced out prior to translation. See also AAN80495-N80496, AAN80499 and AAN80941-2.
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                                                                                                                                                                                                                                                                                                                   Query Match 96.2%; Score 326.2; DB 9; Length 619; Best Local Similarity 97.6%; Pred. No. 9.3e-95; Matches 331; Conservative 0; Mismatches 8; Indels 0;
                                                                                                                                                                                                                                                                                                  Sequence 619 BP; 177 A; 139 C; 134 G; 169 T; 0 other;
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Location/Qualifiers
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                                                                                                    87EP-0117760
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P-PSDB; AAP80894.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human monoclonal antibody specific for a cancer cell membrane
surface antigen - prepd. from a hybridoma obtd. by cell fusion
between human lymphocytes derived from cancer patients and mouse
myeloma cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ë
                                                       Monoclonal antibody; hybridoma; PCR; variable region; constant region; heavy chain; light chain; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tagawa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 342 BP; 88 A; 92 C; 87 G; 75 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGGTGGACGTTCGGCCAAGGGACCAAGGTGAAATCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nagaike K,
GAH variable region of light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 13; Page 31 + 15; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hirakawa Y, Hosokawa S, Ito N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MITU ) MITSUBISHI KASEI CORP
                                                                                                                                                                                                                                                                                                                                                                                                  91JP-0158859.
91JP-0158860.
91JP-0158861.
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                                                                                                                                                                                                                                                                                                                                           92EP-0110841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1993-001328/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAR30144.
                                                                                                                                                                                                                                                                                                                                                                                                  28-JUN-1991;
28-JUN-1991;
28-JUN-1991;
                                                                                                                                                                                                                                                                                                                                           26-JUN-1992;
                                                                                                                                                                                                                                                                             30-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAQ71718
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120 120 180 180

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240 240

(first entry)

06-MAY-1993

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121 AAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lymphocytes were sepd. from regional lymph nodes of a patient who had undergone mastectomy for breast cancer. The Blymphocyte fraction was incubated for 20 hrs with Epstein-Barr virus, then cloned by limiting dilution and tested for immunoadherence. Clones producing antibodies reactive with the UCLA-SO-M12 melanoma cell line were recloned 7 times in serum-free medium contg. growth factors. The resulting L612 is a B-lymphoblastoid cell line transformed by the Epstein-Barr virus. It is deposited at the ATCC under CRL 10724. Humab L612 binds to renal cell carcinomas. The DNA sequence of the variable regions for both the light and heavy chains of the L612 antibody were determined by PCR and are given in AAQ71717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New transformed human B lymphoblastoid cell line - producing monoclonal antibody reactive with GM3 and GM4 ganglioside(s), for treating tumours, esp. melanoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query March
Best Local Similarity 98.5%; Pred. No. 1.5e-92;
Marches 322; Conservative 0; Mismarches 5; Indels C
                                      Monoclonal antibody L612 light chain variable region.
                                                              Immunoglobulin; L612; light chain; variable region; monoclonal antibody; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 360 BP; 88 A; 104 C; 85 G; 83 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 31-32; 39pp; English
                                                                                                                                   Location/Qualifiers
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/label= CDR 1
154.174
/*tag= CDR 2
/label= CDR 2
271..297
                                                                                                                                                                                                                                                                             /*tag= d
/label= CDR 3
                                                                                                                                                                                                                                                                                                                                                                                                       93US-0026320.
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            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                (REGC ) UNIV CALIFORNIA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; AAR61240.
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                                                                                                                                                                                                                                                                                                                                                                           09-FEB-1994;
                                                                                                            Homo sapiens
                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                       26-FEB-1993;
                                                                                                                                                                                                                                                                                                                                                  01-SEP-1994,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Irie RF;
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The invention provides a neuromodulatory agent (I) capable of promoting neurite outgrowth, regeneration, remyelination and neuroprotection in neurite outgrowth, regeneration, remyelination and neuroprotection in promoting cellular proliferation of glial cells, and promoting Ca2+ signaling with oligodendrocytes. An humanised antibody to (I) can be selected from antibody sHGM22 (LMX 22), ebHigM MSI19D10, ebv HIGM CB2bG8, AKGR4, CB21E12, CB21E7 or NSI19E5. (I) is useful for stimulating remyelination of CNS axons, stimulating proliferation of glial cells in CNS axons, or treating demyelinating disease of CNS of such therapy. (I) is capable of binding to structures and cells within CNS axons, or treating demyelinating disease of CNS of a mouse infected with Strain DA of Theiler's murine encephalomyelitis (TMEV) or for treating a human being having multiple sclerosis, or a chuman or domeeric animal with a viral demyelinating disease of CNS (TMEV). (TMEV) (N) is also useful for an in viron method of stimulating the proliferation of glial cells from mixed cell culture.
                                    240
                                                                              312
                                                                                                     241 CAGGCTGAAGATGTGGCCAGTTTATTACTGTCAGCAATATTATAGTACTCCTCCGACGTTC 300
                                  181 CCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neuromodulatory; central nervous system; CNS; sHIGM22; LYM 22; AKJR4; ebvHigM MsI19D10; ebv HIgM CB2bG8; CB2iE12; CB2iE7; MSI19B5; virucide; antiparkinsonian; neuroprotective; nootropic; vulnerary; ds.
CCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTG
                                                                              253 CAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACTCCTCGAACGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                   ebvHigM MSI19D10 light chain variable region nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel neuromodulatory agent (a human IgM monoclonal antibody), promoting neurite outgrowth, regeneration, remyelination and neuroprotection in central nervous system, useful to treat post-infectious encephalomyelitis.
                                                                                                                                                            GGCCAAGGGACCAAGGTGGAAATCAAA 339
                                                                                                                                                                                 301 GGCCAAGGGACCAAGGTGGAAATCAAA 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MAYO-) MAYO FOUND MEDICAL EDUCATION RES
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1..357
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 43; Fig 20; 219pp; English.
                                                                                                                                                                                                                                                                                                  ABA94219 standard; DNA; 357 BP
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                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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P-PSDB; ABB07172.
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                                                                                                                                                                                                                                                                                                                                                                                 13-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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193
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120 132

9 72

Gaps

5; Indels 0;

1 ACCCAGTCTCCAGACTCCCTGGCTGTCTCTGGGCGGGGGGGCCACCATCAACTGCAAG

13 ACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGGGGCCACCATCAACTGCAAG

AAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGGAATCCGGGGTC 192

61 TCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTACCTTGGTACCAGCAG

TCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACTTGGTACCAGCAG

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                              antibodies are useful for preventing infection by a bacterium, virus or like pathogen that causes demyelination or other neurodegenerative condition in a subject. Methods where (I) is administered to a patient are useful for treating multiple sclerosis, Parkinson's disease, Alzheimer's disease, amyotrophic lateral sclerosis (ALS), a viral demyelinating disease, CNS diseases, and other conditions in the CNS
                                                                                                                                                                                                                                                             The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATCAACTGCAAGTCCAGAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAATCCGGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAATCCGGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGGACAGATTTCACTCTCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT
                                                                                                                                                                                                                                                         where nerves are damaged as by trauma. The present sequence represent the ebvHigM MSI19D10 light chain variable region nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
       is also useful for stimulating remyelination of CNS axons. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; colon cancer; colon cancer antigen; diagnosis; detection; defactification; cytostatic; cardioactive; neuroprotective; vulner immunomodulatory; muscular; gynaecological; gastrointestinal; nephrotropic; antiinfective; antibacterial; gene therapy; wound; neural disoxder; immune system disorder; muscular disoxder; reproductive disoxder; qastrointestinal disoxder; reproductive disoxder; cardiovascular disorder; se.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 93.9%; Score 318.2; DB 24; Length 357; Best Local Similarity 96.2%; Pred. No. 2.8e-92; Matches 326; Conservative 0; Mismatches 13; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
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                                                                                                                                                                                                                                                                                                                                                                   Sequence 357 BP; 88 A; 101 C; 86 G; 82 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ВР
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200055351-A1
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called human colon cancer antigens, given in AABS2234 to AABS4066. The human colon cancer antigens can have cytostatic, cardioactive, muscular; neuroprotective, immunomodulatory of antibacterial, gastrointestinal, vulnerary, nephrotropic, antihifective and antibacterial activities, and can be used in gene therapy. The colon cancer antigen polymucleotides, corporation and antibacies to the proteins are useful for the prevention, treatment and diagnosis of colon disorders, such as colon cancer. The polymucleotides may be used in diagnostics and research, such as for chromosome identification, and as hybridisation probes. The proteins may also be used to prevent disorders, reproductive disorders, immune system disorders, muscular disorders, reproductive disorders, immune clastical disorders, wounds, renal disorders, infectious diseases, and cardiovascular disorders, AACS9772 and AACS9772 represent sequences used in the exemplification of the present
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                                            Colon cancer associated gene sequences, referred to as colon cancer antigens, useful for the treatment, prevention, and diagnosis of colon disorders such as colon cancer -
                                                                                                                                                        AAC97991 to AAC98763 encode the human colon cancer associated proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93.0%; Score 315.2; DB 21;
95.3%; Pred. No. 2.8e-91;
iive 0; Mismatches 16;
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                                                                                                                       Claim 1; Page 935; 2104pp; English.
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2000-587534/55.
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nes 323; Conserv
                P-PSDB; AAB53686
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                                                                                                                                                                                                                              The invention relates to producing gene libraries, comprising immunoglobulin light and heavy variable region. The method involves selecting light chain that binds with the heavy chain product to produce a functional conformation, producing a gene library comprising a collection of these light chain variable genes, and combining with gene library of heavy chain variable genes. The method is used for production of gene and antibody libraries.
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                                                                                                                                                     Producing gene libraries and antibody libraries, involves selecting a
light chain that binds to a heavy chain product to produce a functional
formation, and producing a gene library of the light chain variable
                                                                                        Takahashi M;
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                                                                                                                                                                                                                                                                                                                                            Query March 92.9%; Score 315; DB 22; Length 360; Best Local Similarity 95.6%; Pred. No. 3e-91; Marches 324; Conservative 0; Mismatches 15; Indels 0
                                                                                      Shinohara M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
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                                                                                                                                                                                                                                                                                                                       Sequence 360 BP; 89 A; 100 C; 89 G; 82 T; 0 other;
                                                                                      Y, Iba Y, Morino K,
                                                                  CO LTD.
                                                                                                                                                                                                             Examples, p 147-148; 181pp; Japanese.
                                                                 (MEDI-) MEDICAL & BIOLOGICAL LAB
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                     22-FEB-2001; 2001WO-JP01298
                                            2000JP-0050543
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                                                                                     Kurosawa Y, Akahori
Okuno Y, Shiraki K;
                                                                                                                      WPI; 2001-565420/63.
P-PSDB; AAG65565.
                                            22-FEB-2000;
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30-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The plasmid pATGFLAG was generated from pSCFVUHH (see AAQ45605) to incorporate a flag-coating sequence 3' to any human VH gene to be expressed contiguously with Hum4 VL. The plasmid pATGFLAG, when digested with XhoI and Nhe I and purified becomes the human cH discovery plasmid contg. Hum4 VL in this SCFV format. pSC49FLAG contains murine antibody CC49VH inserted into sites of XhoI - he purpose of pATDFLAG. It was evaluated for biological activity with the purpose of serving as a positive control for the FLAG assay
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New composite antibody binding to tumour associated TAG-72 antigen - includes light chain variable region from human subgroup 4 germline gene, useful, opt. as conjugate, for diagnosis or treatment of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1028 BP; 289 A; 226 C; 244 G; 269 T; 0 other;
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                                                                        /note= "ENCODES SIGNAL, H4VL, LINKER see AAR38320 FT"
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/product= flag peptide
Location/Qualifiers
293..775
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P-PSDB; AAR38320, AAR40753.
                                                                                                                                     784..816
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P-PSDB; AAY50693
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20-OCT-1992;
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                                               599
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539
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TAG-72; c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to producing humanized anti-tumor associated sialylated glycoprotein (TAG-72) antibodies (anti-TAG). The antibodies have binding specificity for the cancer antigen TAG-72. These antibodies have variable regions with VL segments derived from human subgroup IV germline gene and a VH segment (encoded by the VHalphaTAG germline gene) which is capapble of combining with the VL to form a threee dimensional structure having the ability to bind TAG-72. They can be used for the in vivo detection of carcinoma lesions. They can also be used for the in vivo diagnostics. They can also be modified with therapeutic agents e.g. a radionuclide, drug, biological response modifier, toxin or another antibody for the treatment of cancers. The humanized anti-TAG-72 antibodies can reduce harmful anti-mouse antibody hypersensitivity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
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                                                                                                                                                                                                                                                                                                                                                                                                                         Production of humanized anti-TAG-72 antibodies, used for the detection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GACATCCAGTTGACCCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GACATCGTGATGACCCAGTCTCCAGACTCCTGGCTGTCTCTGGGCGAGAGGGCCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               419 ATCAACTGCAAGTCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGTACCAGCAGAAACCAGGACAGCCTCCTAAAGCTGCTCATTTACTGGGCATCTACCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                  Tumor associated sialylated glycoprotein; TAG-72; cancer antigen; carcinoma lesion; diagnostic; cancer; antibody; anti-mouse antibody hypersensitivity reaction; ss.
                                                                                                           of Hum4 VL-UNIHOPE linker-FLAG peptide of pATDFLAG
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 92.6%; Score 314; DB 20; Length 1028; Local Similarity 95.6%; Pred. No. 9.7e-91; nes 323; Conservative 0; Mismatches 15; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1028 BP; 289 A; 227 C; 243 G; 269 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                      in vivo imaging and treatment of cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 5; Fig 28A-C; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                             Mezes PS;
                                    ВР
                                  AAZ39437 standard; DNA; 1028
                                                                                                                                                                                                                                                                                  94US-0261354.
90US-0510697.
92US-0964536.
                                                                                                                                                                                                                                                            95US-0487743
                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                            Richard RA,
                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-619651/53.
                                                                                                                                                                                                                                                                                                                                   (DOWC ) DOW CHEM CO.
                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; AAY57184.
                                                                                                             DNA sequence
                                                                                                                                                                                                                                                           07-JUN-1995;
                                                                                                                                                                                                                                                                                    16-JUN-1994;
                                                                                                                                                                                                          US5976845-A.
                                                                                                                                                                                                                                                                                               19-APR-1990;
20-OCT-1992;
                                                                                  29-FEB-2000
                                                                                                                                                                                                                                                                                                                                                             Johnson KS,
                                                                                                                                                                                                                                   02-NOV-1999
                                                                                                                                                                                    Synthetic.
                                                           AAZ39437;
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Matches
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This invention describes novel humanized anti-tumor associated sialylated glycoprotein antibodies (TAG-72) which have cytostatic activity. The antibodies have binding specificity for the cancer antigen TAG-72. They can be used for the in vivo detection of carcinoma lesions. They can also be used for in vitro diagnostics. They can also be modified with therapeutic agents e.g. a radionuclide, drug, biological response modifier, toxin or another antibody for the treatment of cancers. The humanized anti-TAG-72 antibodies can reduce harmful anti-mouse antibody hypersensitivity reactions.
                                                          300
                                                                                                                  658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nntibody, humanized, anti-tumor, sialylated glycoprotein antibody,
cytostatic, cancer antigen, detection, carcinoma lesion,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             359 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTCTCTGGGCGAGAGGGCCACC 418
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                                                                                                  GAATCCGGGGTCCCTGACCGATTCAGTGGCAGGGGTCTGGGACAGATTTCACTCTCACC
                                                          241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New humanized anti-TAG-72 antibodies, used for the detection, in vivo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                               CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAA 338
                                                                                                                                                                                                                                       ccrcrcacrrrcecceaededaccaaegregrearcaa 696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 314; DB 20;
Pred. No. 9.7e-91;
0; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 5; Figure 28A-C; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmid pATDFLAG FLAG DNA adapter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     imaging and treatment of cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diagnostic; treatment; ss
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Best Local Similarity 95.6
Matches 323; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-632731/54.
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GACATCGTGATGACCCCAGTCTCCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC
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                      1 GACATCCAGTTGACCCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC
                                                                               ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCT
                                                                                                                                                               181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGGGGTCTGGGACAGATTTCACTCTCACC
                                                                                                                                                                                                             241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT
                                                                      ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumor associated sialylated glycoprotein; TAG-72; cancer antigen; carcinoma lesion; diagnostic; cancer; antibody; SCFV; anti-mouse antibody hypersensitivity reaction; ss.
                                                                                                                                                                                                                                                                                                                                                                                                              DNA sequence of Hum4 VL-CC49VH SCFV present in pSCFVUIIII
                                                                                                                                                                                                                                                           CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAA 338
                                                                                                                                                                                                                                                                         CCTCTCACTTTCGGCGGACCAAGGTGGTGATCAA 696
15;
Mismatches
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90US-0510697.
92US-0964536.
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 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-619651/53.
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20-OCT-1992;
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323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
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                                                                                          TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
             479 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 538
                                                          GAATCCGGGGTCCCTGACCGATTCAGTGGCGGGTCTGGGGACAGATTTCACTCTCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmid pSCFV UHH expresses a biologically active, TAG-72 binding SCFV consisting of the Hum4 VL and CC49 VH. The expression plasmid utilises the beta-lactamase penP promoter, pectate lyase pelB signal sequence and the penP terminator region. Different Ig light chain variable regions can be inserted in the Ncol-HindIII sites, and different SCFV linkers can be inserted in the HindIII-XhoI sites, and different Ig heavy chain variable regions can be inserted in the XhoI-Nhe I sites.
                                                                                                                                                                                                                                                                                                                 Single chain antibody; SCFV1; human subgroup 4 germline antibody; variable heavy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= a
/note= "ENCODES SIGNAL, H4VL, LINKER, CC49VH (SEE
AAR38319 FT)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 314; DB 14; Length 1330;
Pred. No. 1.1e-90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New composite antibody binding to tumour associated TAG-72 antigen - includes light chain variable region from human subgroup 4 germline gene, useful, opt. as conjugate, for diagnosis or treatment of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1330 BP; 362 A; 300 C; 319 G; 349 T; 0 other;
                                                                                                                                                                                                                                                                                          Sequence of Hum4 VL-CC49VH SCFV present in pSCFVUHH.
                                                                                                                                         CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAA 338
                                                                                                                                                            CTCTCACTTTCGGCGGAGGGACCAAGGTGGTGATCAA 696
                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
293..1117
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                                                                                                                                                                                                                         BP.
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                                                                                                                                                                                                                                                                     (first entry)
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P-PSDB; AAR38319.
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Best Local Similarity
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The invention relates to producing humanized anti-tumor associated sialylated glycoprotein (TAG-72) antibodies (anti-TAG). The antibodies have binding specificity for the cancer antigen TAG-72. These antibodies have variable regions with VL segments derived from human subgroup IV germline gene and a VH segment (encoded by the VHalphaTAG germline gene) which is capaphle of combining with the VL to form a three dimensional structure having the ability to bind TAG-72. They can be used for the in vivo detection of carcinoma lesions. They can also be used for in vitro
Production of humanized anti-TAG-72 antibodies, used for the detection, in vivo imaging and treatment of cancers
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13-DEC-1991;
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                                                                                                                                                                                                                          GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCCACC
                                                                                                                                                                                                                                                               GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTCTCTGGGCGAGAGGGCCACC
                                                                                                                                                                                                                                                                                                    ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT
                                                                                                                                                                                                                                                                                                                           TGGTACCAGCAGAAACCAGGACAGCCTCCTAAAGCTGCTCATTTACTGGGCATCTACCCGG
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                                                                                                                                                                                          Gaps
diagnostics. They can also be modified with therapeutic agents e.g. radionucliade, drug, biological response modifier, toxin or another antibody for the treatment of cancers. The humanized anti-TAG-72 antibodies can reduce harmful anti-mouse antibody hypersensitivity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New humanized anti-TAG-72 antibodies, used for the detection, in
                                                                                                                                                                                          ö
                                                                                                                                                   Length 1330;
                                                                                                                                                                                          Indels
                                                                                                                Seguence 1330 BP; 362 A; 302 C; 317 G; 349 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAA 338
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                                                                                                                                                   Score 314; DB 20;
Pred. No. 1.1e-90;
                                                                                                                                                                                        0; Mismatches
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                                                                                                                                                   Query Match
Best Local Similarity 95.6%;
Matches 323; Conservative
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Best Local Similarity
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538
This invention describes novel humanized anti-tumor associated sialylated glycoprotein antibodies (TAG-72) which have cytostatic activity. The antibodies have binding specificity for the cancer antigen TAG-72. They can be used for the in vivo detection of carcinoma lesions. They can also be used for in vitro diagnostics. They can also be modified with therapeutic agents e.g. a radionuclide, drug, biological response modifier, toxin or another antibody for the treatment of cancers. The humanized anti-TAG-72 antibodies can reduce harmful anti-mouse antibody
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Single chain antibody; SCFV1; human subgroup 4 germline antibody; variable heavy; ss.
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/note= "ENCODES SIGNAL, HV4L, LINKER, CC49VH, FLAG
- SEE AAR38321 FT"
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                                                                                                                                                                                                                                                                                                                            Length 1330;
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                                                                                                                                                                                                                                                                        C; 317 G; 349 T; 0 other;
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                                                                                                                                                                                                                                                                                                                       Score 314; DB 20;
Pred. No. 1.1e-90;
0; Mismatches 15;
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                                                                                                                                                                                                                                                                        Sequence 1330 BP; 362 A; 302
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Conservative
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                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 323; Conserv
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                                                                                                                                                                                                                                           The plasmid pATGFLAG was generated from pSCFVUHH (see AAQ45605) to incorporate a flag-coating sequence 3' to any human VH gene to be expressed contiguously with Hum4 VL. The plasmid pATGFLAG, when digested with XhoI and Nhe I and purified becomes the human chi discovery plasmid coneg. Hum4 VL in this SCFV format. pSC49FLAG contains murine antibody CC49VH inserted into sites of XhoI - NheI purpose of pATGFLAG. It was evaluated for biological activity with the purpose of serving as a positive control for the FLAG assay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 92.6%; Score 314; DB 14; Length 1359; Best Local Similarity 95.6%; Pred. No. 1.1e-90; Matches 323; Conservative 0; Mismatches 15; Indels 0;
                                                                                                  New composite antibody binding to tumour associated TAG-72 antigen - includes light chain variable region from human subgroup 4 germline gene, useful, opt. as conjugate, for diagnosis or treatment of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1359 BP; 374 A; 308 C; 325 G; 352 T; 0 other;
  Richard RA
                                                                                                                                                                                                       Example, Figure 30, 150pp, English
  Mezes PS,
                                        WPI; 1993-214173/26.
N-PSDB; AAQ44607.
  Johnson KS,
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CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAA 338 ccrcrcacrircegegegegeceaegeregrearcaa 696

Search completed: July 18, 2003, 06:44:05 Job time : 88.8822 secs

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Sequence 453, App
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8533.875 Million cell updates/sec
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Sequence 2
Sequence 5
Sequence 2
Sequence 3
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1: \cgn2_6/ptodata/1/pubpna/US07 PUBCOMB.seq:*
2: \cgn2_6/ptodata/1/pubpna/PCT NEW PUB.seq:*
3: \cgn2_6/ptodata/1/pubpna/PCT NEW PUB.seq:*
4: \cgn2_6/ptodata/1/pubpna/US06_NEW PUB.seq:*
5: \cgn2_6/ptodata/1/pubpna/US06_NEW PUB.seq:*
6: \cgn2_6/ptodata/1/pubpna/US08_NEW PUB.seq:*
7: \cgn2_6/ptodata/1/pubpna/US08_NEW PUB.seq:*
9: \cgn2_6/ptodata/1/pubpna/US08_NEW PUB.seq:*
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10: \cgn2_6/ptodata/1/pubpna/US09_NEW PUB.seq:*
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15: \cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
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GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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US-09-897-511A-34
US-09-997-511A-34
US-09-274-163E-1
US-09-274-163E-3
US-09-187-693-22
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US-09-187-693-24
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Maximum Match 100%
Listing first 45 summaries
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Match I
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311.8
311.8
305.2
303.3
300.4
294.4
292.6
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288
280.2
279
276.4
273.4
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database
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Sequence 28, Appl Sequence 112, App Sequence 409, Appl Sequence 409, Appl Sequence 409, Appl Sequence 5, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 57, Appli Sequence 57, Appli Sequence 57, Appli Sequence 77, Appli Sequence 10, Appli Sequence 5, Appli	'n'n
US-09-187-693-28 . US-09-828-708-112 US-09-828-708-112 US-09-604-287A-409 US-09-551-621-409 US-09-551-621-409 US-10-121-464-1 US-10-121-464-1 US-10-121-464-1 US-10-121-464-1 US-10-198-846-136-29 US-10-198-846-136-29 US-10-198-846-136-29 US-09-998-831-8 US-09-998-831-8 US-09-998-831-8 US-09-998-831-8 US-09-998-91-7 US-09-995-693-3 US-09-995-693-3 US-09-995-693-3 US-09-995-693-3 US-09-995-6-087-1	39-791-
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ALIGNMENTS

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WESULT No. US20202055627A1
Sequence 453, Application US/09925299
Patent No. US202020055627A1
Sequence 453, Application US/09925299
Patent No. US202020055627A1
TITLE OF INVENTANION NUMBER: US/09/925,299
CURRENT PILION DATE: 2001-08-10
PRIOR PRICATION NUMBER: US/09/925,299
CURRENT PAPLICATION NUMBER: US/09/925,299
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR PILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOCTHARE: PatentIn Ver: 2.0
PROGANISM: Misc feature
LOCATION: (315)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (315)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (315)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (314)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (404)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (4155)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (4155)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (4155)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (4155)
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NAME/KEY: misc feature
LOCATION: (4155)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (4155)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (4155)
OTHER INFORMATION: n equals a,t,g, or c
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186

246

306

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TITLE OF INVENTION: Immunoglobulin Superfamily Polynucleotides, Polypeptides, and All TITLE OF INVENTION: Immunoglobulin Superfamily Polynucleotides, Polypeptides, and All TITLE OF INVENTION Immunoglobulin Superfamily Polynucleotides, Polypeptides, and CURRENT APPLICATION NUMBER: US/09/799,514
CURRENT FILING DATE: 2001-03-07
PRIOR FILING DATE: 2000-08-29
PRIOR FILING DATE: 1999-00-03
PRIOR FILING DATE: 1999-09-03
NUMBER OF EQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                     127 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAATAAGAACTACTTAAACT
                                                                                                                                                                                                                                                                                                                                            247 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC
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                                                                                  187 TGGTACCAGCAGAACCAGGACAGCCTCCTAAGCTGCTCCTTTACTGGGCATCTACCCGG
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92.0%; Score 311.8; DB 10; Length
Best Local Similarity 95.0%; Pred. No. 5.9e-97;
Matches 322; Conservative 0; Mismatches 17; Indels
al Similarity 95.3%; Pred. No. 2.8e-98; 323; Conservative 0; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301.CCTCGAACGTTCGGCCAAGGACCAAGGTGGAAATCAAA 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 3
US-09-799-514-2
i Sequence 2, Application US/09799514
i Patent No. US2002065220A1
i GENERAL INFORMATION:
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US-09-799-514-2
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Best Local
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                                                                                                                                                      61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
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                                         Length 463;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERNCE: PA102
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT APPLICATION NUMBER: US/09/983
PRIOR APPLICATION NUMBER: POT/US00/05883
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARR: PatentIn Ver. 2.0
SEQ ID NO 453
LENGTH: 463
                                         Score 315.2; DB 10; Length
Pred. No. 2.8e-98;
0; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      367 CCCTGGACGTTCGGCCACTGGACCAANGTGGAAATCANA 405
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (315)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (393)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (404)
LOCATION: (404)
LOCATION: (404)
LOCATION: (404)
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; Publication No. US20030040617A9
; GENERAL INFORMATION:
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OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
LOCATION: (435)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
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US-09-925-299-453
                                  Query Match
Best Local Similarity 95.3%;
Matches 323; Conservative
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US-09-925-299-453
US-09-925-299-453
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US-09-897-006-34
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Patent No. US2002017362941
GENERAL INFORMATION:
APPLICANT: Jakobowits, Aya
APPLICANT: Yang, Xiao-Dong
APPLICANT: Jan, Xiao-Chi
TITLE OF INVENTION: Human Monoclonal Antibodies to Epidermal
TITLE OF INVENTION: Growth Factor Receptor
FILE REFERENCE: Cell 4.20 CIP2
CURRENT APPLICATION NUMBER: US/09/187,693
CURRENT FILING DATE: 1998-11-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030073105A1 1101440.8
US-10-158-646-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match '90.0%; Score 305.2; DB 15; Length Best Local Similarity 95.3%; Pred. No. 9.8e-95; Matches 326; Conservative 0; Mismatches 13; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           382 crcccccrcacrircecccaaccaaccaaccaacacacaaa 423
                                                                                                                    Sequence 58, Application US/10158646

Publication No. US20030073105A1

GENERAL INFORMATION:
APPLICANT: Lasek, Amy K.W.
TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
FILE REFERENCE: PA-0030 US
CURRENT APPLICATION NUMBER: US/10/158,646

CURRENT APPLICATION NUMBER: 02/2-29

PRIOR FILING DATE: 2001-05-31

NUMBER OF SEQ ID NOS: 78

SOFTWARE: PERL PROGRAM

SEQ ID NOS: 78

LENGTH: 788
                         301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
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US-09-187-693-26
                                                                                                                US-10-158-646-58
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95.4%; Pred. No. 4.4e-94;
tive 0; Mismatches 15;
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PRIOR APPLICATION NUMBER: 09/162,280
PRIOR FILING DATE: 1980-09-29
PRIOR PILING DATE: 1987-05-25
NUMBER OF SEQ ID NOS: 75
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 26
LENGTH: 463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: (1)...(463)
CTHER INFORMATION: n = A,T,C or G
US-09-187-693-26
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ORGANISM: Artificial Sequence
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Best Local Similarity 95.4
Matches 312; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: human
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241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
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Fatent No. US2020137897A1
Fatent No. US2020137897A1
FAPPLICANT: WILKINS STEVENS, Fred J.
APPLICANT: WILKINS STEVENS, Priscilla
APPLICANT: RAFFER, Marianne
TITLE OF INVENTION: OPTITUM RECOMBINANT ANTIBODY PRODUCTION
FILE REFERENCE: 051583/0224 RECOMBINANT APPLICATION NUMBER: US 08/373,380
FRIOR FILING DATE: 1995-01-17
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 86.8%; Score 294.4; DB 12; Length Best Local Similarity 98.0%; Pred. No. 3.4e-91; Matches 298; Conservative 0; Mismatches 6; Indels
                                                                                         RESULT 8

US-09-995-529-5

US-08-095-529-5

Publication No. US2003009655A1

Fublication No. US2003009655A1

GRARRAL INFORMATION:

APPLICANT: Huse, William D.

APPLICANT: Tang, Ying

TITLE OF INVENTION: Humanized Collagen Antibodies and

TITLE REFERENCE: P-IX 4976

CURRENT APPLICATION NUMBER: US/09/995,529

CURRENT APPLICATION NUMBER: US/09/995,529

NUMBER OF SEQ ID NOS: 358

SEQ ID NO S

SEQ ID NO S

LENGTH: 305
                             6000 GACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 6033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-995-529-5
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US-09-274-163E-1
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5703 CGAGCTCACCCAGTCTCCAGACTCCCTGGCTGTCTCTGGGCGAGAGGGCCACCATCAA 5762
                                                                                   CCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGGAATCTACCGGGAAATC 185
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Sequence 34, Application US/09897511A

Publication No. US2003092882A1

Publication No. US2003092882A1

SEQID NO 34

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                                               CTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACTTGGTA
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88.6%; Score 300.4; DB 12; Length 9511;
Best Local Similarity 95.8%; Pred. No. 1.4e.92;
Matches 320; Conservative 0; Mismatches 11; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                    306 AACGTTCGGCCAAGGACCAAGGTGGAAATCAAA 339
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Synthetic US-09-897-511A-34
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                                                                                    181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
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                61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACTCTAAGAACTACTTAGCT 120
                                                                                                                                                                                                                                                241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
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                                                              TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG
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; Patent No. US20020137897A1
; Fatent No. US20020137897A1
; GENERAL INFORMATION:
; APPLICANT: STEVENS, Fred J.
; APPLICANT: MILKINS STEVENS, Priscilla
APPLICANT: RAFFEN, Rosemarie
; APPLICANT: SCHIFFER, Marianne
; TITLE OF INVERTION: OPTIMUM RECOMBINANT ANTIBODY PRODUCTION
; TITLE OF INVERTION: OPTIMUM RECOMBINANT ANTIBODY PRODUCTION
; CURRENT APPLICATION NUMBER: US/09/274,163E
; CURRENT FILING DATE: 1999-03-22
; PRIOR FILING DATE: 1995-01-17
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Version 3.1
; FROUTH OS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 85.8%; Score 291; DB 11; Length 343; Best Local Similarity 91.2%; Pred. No. 5.3e-90; Matches 309; Conservative 0; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                       301 ccgracrccrrccgcrcaccaaccrccaaarcaaa 339
                                                                                                                                                                                                                                                                                                                                           CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
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, OTHER INFORMATION:
US-09-274-163E-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
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Patent No. US2020137897A1

GENERAL INFORMATION:

APPLICANT: STEVENS, Fred J.

APPLICANT: STEVENS, Fred J.

APPLICANT: RAFFEN, MARIANNE

TITLE OF INVENTION: OPTIMUM RECOMBINANT ANTIBODY PRODUCTION

FILE REFERENCE: 051583/0224

CURRENT APPLICATION NUMBER: US/09/274,163E

CURRENT FILING DATE: 1999-03-22

PRIOR PRILING DATE: 1995-01-17

NUMBER OF SEQ ID NOS: 16

SOFTWARE: Patentin version 3.1

SEQ ID NO 3

LENGTH: 343
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.larity 91.2%; Pred. No. 5.3e-90;
Conservative 0; Mismatches 30; Indels
                                                                                                                                                         Score 292.6; DB 11; Pred. No. 1.5e-90; Indels
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                                                                                                                                                                          Query Match

86.3%; Score 292.6; Sest Local Similarity 91.4%; Pred. No. 1.5e
Matches 310; Conservative 0; Mismatches
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(342)
; OTHER INFORMATION:
US-09-274-1638-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Escherichia coli
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LOCATION: (1)..(342)
CTHER INFORMATION:
US-09-274-163E-3
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Best Local Similarity
Matches 309; Conserv
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US-09-274-163E-3
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US-09-187-639-24

1 Sequence 24, Application US/09187693

Patent No US2002013629A1

SERERAL INFORMATION:
APPLICANT: Jakobovits, Aya

APPLICANT: Jakobovits, Aya

APPLICANT: Jakobovits, Aya

APPLICANT: Jai, Xiao-Chi

TILLE OF INVENTION: Human Monoclonal Antibodies to Epidermal

TILLE OF INVENTION: Human MONOCLONAL SECPETOR

TILLE OF INVENTION: Human MONOCLONAL SECPETOR

TILLE OF INVENTION HUMBER: US/09/187,693

PRIOR APPLICATION NUMBER: 09/162,280

PRIOR APPLICATION NUMBER: 09/162,280

PRIOR PELING DATE: 1998-09-29

PRIOR PILING DATE: 1998-09-29

PRIOR PILING DATE: 1999-05-05

NUMBER OF SEC ID NOS: 75

SOFTWARE: FastSEC for Windows Version 4.0

LENGTH: 456
PRIOR APPLICATION NUMBER: 09/162,280
PRIOR FILING DATE: 1998-09-29
PRIOR APPLICATION NUMBER: 08/851,362
PRIOR FILING DATE: 1997-05-05
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PASTSEQ for Windows Version 4.0
LENGTH: 460
                                                                                                                                                                                            FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(460)
OTHER INFORMATION: n = A,T,C or G
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NAME/KRS: misc_feature
LOCATION: (1) ... (456)
OTHER INFORMATION: n = A,T,C or
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                                                                                                                                                      TYPE: DNA
ORGANISM: human
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ORGANISM: human
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Best Local Similarity 92.4%; Pred. No. 1e-88;
Matches 314; Conservative 0; Mismatches 25; Indels 1; Gaps
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OTHER INFORMATION: Incyte ID No. US20030073105A1 1101440.15
FEATURE:
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Retent No. US20020173629A1

RETENT OF US20020173629A1

APPLICANT: Jakobovits, Aya

APPLICANT: Yang, Xiao-Dong

APPLICANT: Gallo, Michael

APPLICANT: Gi, Xiao-Chi

TITLE OF INVENTION: Growth Factor Receptor

FILE REFERENCE: Cell 4.20 C1P2

CURRENT APPLICANI NUMBER: US/09/187,693

CURRENT FILING DATE: 1998-11-05
       RESULT 12
US-10-158-646-59
US-10-158-646-59
Sequence 59, Application US/10158646
Publication No. US20030073105A1
GENERAL INPORMATION:
TILLE OF LIVERINT SCRIASSE, Thierry
TILLE OF INVENTION: GENER SEPRESSED IN COLON CANCER
FILE REFRENCE: PA-0030-1 US
CURRENT APPLICATION NUMBER: US/10/158,646
PRIOR APPLICATION NUMBER: US/10/158,646
PRIOR APPLICATION NUMBER: G/295,239
PRIOR APPLICATION NUMBER: G/295,239
NUMBER OF SEQ ID NG 59:78
SEQ ID NG 59:78
LENGTH: 1230
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1. LOCATION: 1143-1160

OTHER INFORMATION: a, t, c, g, or other

US-10-158-646-59
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ORGANISM: Homo sapiens
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US-09-187-693-22
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US-09-187-693-30.

i Sequence 30, Application US/09187693

sequence 30, Application US/09187693

sequence 30, Application US/09187693

sequence 30, Application US/09187693

sequence 30, Application US/09187693

sequence 30, Application Application Applicant January Applicant January Applicant January Applicant January Michael Applicant January Michael Applicant January Michael January January Michael January January Horizon Human Monoclonal Antibodies to Epidermal TITLE OF INVENTION: Human Monoclonal Antibodies to Epidermal TITLE OF INVENTION: Human Monoclonal Antibodies to Epidermal TITLE OF INVENTION NUMBER: US/09/187,693

CURRENT FILING DATE: 1998-09-29

PRIOR APPLICATION NUMBER: 08/951,362

PRIOR APPLICATION NUMBER: 08/951,362

NUMBER OF SEQ ID NOS: 75

SEQ ID NO 30

LENGTH: 476
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                                                                                              82.3%; Score 279; DB 11; Length 456; 93.2%; Pred. No. 8.3e-86; ive 0; Mismatches 21; Indels
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; OTHER INFORMATION: n = A,T,C or G
US-09-187-693-30
                                                                                      Query Match
Best Local Similarity 93.2'
Matches 302; Conservative
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ORGANISM: human
US-09-187-693-24
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.: /cgn2_6/ptodata1/ina/6A_COMB.seq:*
.: /cgn2_6/ptodata1/ina/6B_COMB.seq:*
.: /cgn2_6/ptodata1/ina/RB_COMB.seq:*
.: /cgn2_6/ptodata1/ina/PCTUS_COMB.seq:*
.: /cgn2_6/ptodata1/ina/Packfiles1.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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339 1 US-08-667-769A-20 Sequence 20,	2 US-08-940-371-20 Sequence	3 US-08-637-647-20 Sequence	S PCT-US95-17082A-20 Sequence	1 US-08-467-420A-50 Sequence	1 US-08-470-110A-50 . Sequence	1 US-08-667-769A-50 Sequence	2 US-08-940-371-50 Sequence	3 US-08-637-647-50 Sequence	Sequence	4 US-09-301-593-5 Sequence	4 US-09-301-593-103 Sequence 103	5 PCT-US93-08435-3 Seguence 3,	4 US-09-301-593-1 Seguence 1,	4 US-09-301-593-31 Sequence 31	8068 4 US-09-301-593-35 Sequence 35, Appl	3 US-08-724-752-7 Sequence 7,	
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ALIGNMENTS

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US-08-360-125-

Begenene A Application US/08360125

Patent No. 576746

FRIENAL INFORMATION:

PAPLICATT: Saich HOSOKAWA

APPLICANT: Tofalaki TraGAWA

APPLICANT: Tofalaki TraGAWA

APPLICANT: Tofalaki TraGAWA

APPLICANT: Washington No. 5767346ihiko ITO

APPLICANT: Washington NaAnike

TITLE OF INVENTION: Human Monoclonal Antibody

TITLE OF INVENTION: Human Monoclonal Antibody

TITLE OF INVENTION: Human Monoclonal Antibody

TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer

NUMBER OF SEQUENCES. 42

CORRESPONDENCE ADRESS:

CORRESPONDENCE ADRESS:

CORRESPONDENCE ADRESS:

CORPETE READABLE FORM:

MEDIUM YER: 10.8 A.

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM YER: 10.8 A.

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM YER: 10.8 A.

ZIP: 20005

CORPETE: 10.8 Compatible

OPERATION SUMBER: 07/905,534

REPLICATION UNBER: 07/905,534

REPLICATION NUMBER: 07/905,534

REPLICATION NUMBER: 07/905,534

REPLICATION NUMBER: 07/905,534

REPLICATION NUMBER: 07/905,534

REPLECOMMUTATION INFORMATION:

TELECOMMUTATION INFORMATION:

TELECOMMUTATION INFORMATION:

TELECOMMUTATION UNPERS: 33,567

REFERENCE POCKETITION OF SEC ID NO: 4:

SEQUENCE CHARACTERISTICS:

INFORMATION TO SEC ID NO: 4:

SEQUENCE CHARACTERISTICS:

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APPLICANT: Saiko HISOKAWA
APPLICANT: Toshiaki TAGAWA
APPLICANT: Toshiaki TAGAWA
APPLICANT: Toshiaki TAGAWA
APPLICANT: Toshiaki TAGAWA
APPLICANT: No. 5837845hiko ITO
APPLICANT: No. 5837845hiko ITO
APPLICANT: No. 5837845hiko ITO
APPLICANT: No. 5837845hiko ITO
APPLICANT: Raubalir Nomen
ITILE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
ITILE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
ITILE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
ITILE OF INVENTION: Call Membrane
NUMBER OF SEQUENCES: Call Membrane
NUMBER OF SEQUENCES: ADDRESS:
ADDRESSEE: Wender-toth Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STREET: Book Fifteenth Street, S. 25 inch, S00 kb
COMPUTER: Diskette, S. 25 inch, S00 kb
COMPUTER: Wordberfect S. 1995
COMPUTER: Wordberfect S. 1995
SOFTWARE: Wordberfect S. 1995
CLASSIFICATION NUMBER: US/09/450,578
FILING DATE: Wordberfect S. 1995
FILING DATE: Une NUMBER: 31,367
REGISTRATION NUMBER: 33,367
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER: 31,367
TELEDRAX:
TELEDRAX:
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FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
INDIVIDUAL ISOLATE:
HAPLOTYPE:
TISSUE TYPE:
TISSUE TYPE:
CELL TYPE:
ANDIA SOURCE:
ORGANELLE:
IMMEDIATE SOURCE:
LINE:
ORGANELLE:
CLONE:
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CHROMOSOME/SEGMENT:
MAP POSITION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 342 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL:
  GENERAL INFORMATION:
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          ANTI-SENSE
PRACHENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
HAPLOTYPE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
HAPP POSTION:
MAP POSTION:
HAPP POSTION:
HAPP POSTION:
OFFER INFORMATION:
PUBLICATION
PUBLICATION
AUTHORS:
AUTHORS:
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FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-360-125-4
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US-08-450-578-4
; Sequence 4, Application US/08450578
; Patent No. 5837845
HYPOTHETICAL:
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LOCATION: IDENTIFICATION METHOD: OTHER INFORMATION:

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241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
                                                                                                                        61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAACTCCAACATAAGAAATACTTAGCT 120
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Patent No. 5990297
GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA et al.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY
TITLE OF INVENTION: BINDING TO SURFACE ANTIGEN OF CANCER CELL MEMBRANE
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
                                                                                                                                                                                                                                                  1 GACATCGTGATGACCCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC
                                                                                                                                                          121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/014,880
FILING DATE: January 28, 1998
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CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/450,578
FILING DATE: May 25, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/360,125
                     GACATCCAGTTGACCCAGTCTCCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: December 20, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
ATTORNEY/ACENT INFORMATION:
RACESTRATION NUMBER: 33,367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
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TYPE: nucleic acid
STRANDEDNESS: double
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 2033 K SI
CITY: Washington
STATE: D.C.
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: U.S.A.
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; OTHER INFORMATION: Hybridoma producing human antibody GAH
US-09-017-628-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
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Pred. No. 2.9e-97;
0; Mismatches 11;
                                                                                                                                   DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                              94.8%;
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PUBLICATION INFORMATION AUTHORS:
                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 328; Conserv
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Matches 328; Conserv
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ORGANISM: Unknown
                                      TITLE:
JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 3
US-09-017-628-4
                                                                                                                                                                                                            US-08-450-578-4
                                                                   VOLUME:
ISSUE:
PAGES:
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61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAACTCCAACAATAAGAAATACTTAGCT 120
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STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
TESUE TYPE:
CELL TYPE:
ORGANELLE:
INMEDIATE SOURCE:
LIBRARY:
CHOWS:
POSITION IN GENOME:
CHOWS:
POSITION IN GENOME:
CHOWSOME (SEGMENT:
MAP POSITION:
UNITS:
DOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
PUBLICATION INFORMATION:
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; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
US-08-450-363-4
NAME: Warren M. Cheek, Jr.
REGISTRATION UNDHER:
REPERENCE/DOCKET UNDHER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEPHONE: 202-371-8850
TELEPHONE: 202-371-8850
TELEPK:
INFORMATION FREQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 342 Base pairs
TYPE: nucleic acid
STRANDENESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL:
ANTI-SENSE:
RAGMENT TYPE:
ORIGINAL SOURCE:
ORIGINAL SOURCE:
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JSEQUENCE 4. Application US/08450363

Patent No. 6436434

GENERAL INFORMATION:

APPLICANT: Saiko HOSOKAWA

APPLICANT: Tobitaki TAGAWA

APPLICANT: No. 6436434iniko ITO

CITTLE OF INVENTION: Cell Membrane

NUMBER OF SEQUENCES: 42

ADDRESSEE: Wenderoth, Lind & Ponack

STATE: 0005

CONBUTER: BOS Fifteenth Street, N.W., #700

CITY: Washington

STATE: Diskette, 5.25 inch, 500 kb

COMPUTER: IBM Compatible

OPERATING SYSTEM: MS. 2006

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION NUMBER: US/08/450,363

FILING DATE: MAY 25, 1995

PRIOR APPLICATION NUMBER: 08/360,125

FILING DATE: December 20, 1994

PRIOR APPLICATION NUMBER: 07/905,534

FILING DATE: June 29, 1992

ATTONEY/AGENT INFORMATION:
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                                                                                                                                                                                     Length 342;
                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                               Query Match 94.8%; Score 321.4; DB 2; Best Local Similarity 96.8%; Pred. No. 2.9e-97; Matches 328; Conservative 0; Mismatches 11;
     TOPOLOGY: linear
MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
CELL TYPE: Hybridoma producing human
CELL TYPE: antibody GAH
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Query Match
Best Local Simi
Matches 323;
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                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: ITIA. Reiko F
APPLICANT: ITIA. Reiko F
TITLE OF INVENTION: HUMAN B-LYMPHOBLASTOID CELL LINE
TITLE OF INVENTION: SECRETING ANTI-GANGLIOSIDE ANTIBODY
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Poms, Smith, Lande & Rose
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                                                                                                                                                          301 ccgrccacccaaccaaccaaccaaccaaarcaaa 339
                                                                                                               301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
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determining region 1 (CDR1)"
                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Poms, Smith, Lande & Rose
2029 Century Park East, Suite 3800
                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 2029 Century Park East, Suite CITY: Los Angeles STATE: California COUNTRY: United States of America ZIP: 90067
COMPUTRY: United States of America ZIP: 90067
COMPUTER: READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Wordferfect 5.1
CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/026,320A FILING DATE: 26-FEB-1993
CLASSIFICATION: 424
PRIOR APPLICATION: 424
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/609803
ATTORNEY/AGENT INFORMATION: NAME: Oldenkamp, David J
7. # 241 ATCAGCAGCCTGCAGGCTGAAGATG
                                                                                                                                                                                                                                            US-08-026-320A-3
; Sequence 3, Application US/08026320A
; Patent No. 5419904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 9426
TELECOMMUNICATION INFORMATION:
TELEFAX: 3107885046
TELEFAX: 310771297
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
LENGTH: 360 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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LOCATION: 58.108
OTHER INFORMATION: /func'
OTHER INFORMATION: detern
FEATURE:
NAME/KEY: misc_feature
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INDIVIDUAL ISOLATE: Epst
INDIVIDUAL ISOLATE: cell
CELL TYPE: B-cell
CELL LINE: L612
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MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
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OTHER INFORMATION:
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NAME/KEY:
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APPLICANT: Richard, Ruth A.
APPLICANT: Richard, Ruth A.
APPLICANT: Richard, Joseph A.
APPLICANT: Kaffolter, Joseph A.
APPLICANT: Kaffolter, Joseph A.
APPLICANT: Kaffolter, Joseph A.
APPLICANT: Kaffolter, Joseph A.
TITLE OF INVENITON: Dimer and Multimer Forms of Single Chain Polypeptides
FILE REFERENCE: 40224A US
CURRENT FILING DATE: 1995-06-05
EARLIER APPLICATION NUMBER: US 07/935,695
EARLIER FILING DATE: 1992-08-21
NUMBER OF SEQ ID NOS: 102
SOFTWARE: MS-Word for Windows, Ver. 7.0
LENGTH: 1330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73 TCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACTTGGTACCAGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                133 AAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                        13 ACCCAGTCTCCAGACTCCCTGGCTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAG
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                                                                                                                                                                                                                                                                                               Query Match 94.1%; Score 319; DB 1; Length 360; Best Local Similarity 98.5%; Pred. No. 1.9e-96; Matches 322; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                /function= "Complementary
determining region 3 (CDR3)"
                                  /function= "Complementary
determining region 2 (CDR2)"
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Pred. No. 1.6e-94;
0; Mismatches 15;
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NAME/KEX:

NAME/KEX:

LOGATION: 1..1330
US-08-463-903-5
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ilarity 95.6%;
Conservative
                                                                                      FEATURE:

NAME/KEY: misc_feature

COCATION: 271...297

OTHER INFORMATION: /funct

COTHER INFORMATION: detern

US-08-026-320A-3
LOCATION: 154..174
OTHER INFORMATION:
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US-00-L1 3
US-00-L1 463-903-19
US-00-L2 463-903-19
Sequence 19, Application US/08463903
Sequence 19, Application US/08463903
Sequence 19, Application US/08463903
Sequence 19, Application US/08463903
GENERAL INFORMATION:
APPLICANT: Michard, Witch A.
APPLICANT: Richard, Witch A.
APPLICANT: Michard, Witch A.
APPLICANT: Michard A.
TILE REFERENCE: 40224 US
FILE REFERENCE: 40224 US
CURRENT APPLICATION WUBBER: US/08/463,903
CURRENT FILING DATE: 1995-06-05
EARLIER APPLICATION WUBBER: US 07/935,695
EARLIER PILING DATE: 1992-08-21
NUMBER OF SEQ ID NOS: 102
SOFTWARE MS-Word for Windows, Ver. 7.0
SEQ ID NO 19
LENGTH: 1027
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Sequence 19, Application US/07935695
Beaten No. 6329507
GENERAL INFORMATION:
APPLICANT: Michael Related, Ruth A.
APPLICANT: Richard, Ruth A.
APPLICANT: Refiber, Joseph A.
APPLICANT: Retite, Nicolas J.
TITLE OF INVENTION: Dimer and Multimer Forms of Single Chain Polypeptides
FILE REFERENCE: 402244 US
CURRENT FILING DATE: 1992-08-13
PRIOR APPLICATION NUMBER: US 08/463,903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 539 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGGGGTCTGGGACAGATTTCACTCTCACC
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ORGANISM: Artificial Sequence
FRATURE:
NAME/KEX: Hum4 VL-UNIHOPE linker-FLAG peptide construct in pATDFLAG
LOCATION: 1..1027
US-08-463-903-19
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92.2%; Score 312.4; DB 3; Length 1027;
Best Local Similarity 95.3%; Pred. No. 4.7e-94;
Matches 322; Conservative 0; Mismatches 16; Indels 0;
659 CCTCTCACTTTCGGCGGAGCGACCAAGGTGGTGATCAA 696
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APPLICANT: Richard, Ruth A.
APPLICANT: Richard, Ruth A.
APPLICANT: Affholter, Joseph A.
APPLICANT: Affholter, Joseph A.
APPLICANT: Affholter, Joseph A.
TITLE OF INVENTION: Dimer and Multimer Forms of Single Chain Polypeptides
FILE REFERENCE: 40224A us.
CURRENT FILING DATE: 1992-08-21
CURRENT APPLICATION NUMBER: US 08/463,903
PRIOR FILING DATE: 1995-06-05
NUMBER OF SEQ ID NOS: 102
SOFTWARE: MS-Word for Windows, Ver. 7.0
SEQ ID NO 5
LENGTH: 1330
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LOCATION: 1..1330
CTHER INFORMATION: :
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Query Match
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APPLICANT: Mezes, Peter S.
APPLICANT: Richard, Ruth A.
APPLICANT: Affholter, Joseph A.
APPLICANT: Affholter, Joseph A.
APPLICANT: Affholter, Oseph A.
TITLE OF INVENTION: Dimer and Multimer Forms of Single Chain Polypeptides
FILE REPERENCE: 40224A US
CURRENT APPLICATION NUMBER: US/08/463,903
EARLIER APPLICATION NUMBER: US 07/935,695
EARLIER FILING DATE: 1992-08-21
NUMBER OF SEQ ID NOS: 102
SOFTWARE: MS-Word for Windows, Ver. 7.0
                                                                                                                                                                                                                                                                                                          1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC
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PRIOR FILING DATE: 1995-06-05
NUMBER OF SEQ ID NOS: 102
SOFTWARE: MS-word for Windows, Ver. 7.0
SEQ ID NO 19
LENGTH: 1027
TYPE: DNA
ORGANISM: Artificial Sequence
FRATURE:
NAME: KEX: Hum4 VL-UNIHOPE linker-FLAG peptide construct in pATDFLAG
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Pred. No. 6.2e-93;
0; Mismatches 18; Indels 0;
                                                                                                                                                                                                                Length 1027;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 21, Application US/08463903 Patent No. 6071515
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Best Local Similarity 94.7%;
Matches 320; Conservative
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                                                                                                                                                                , OTHER INFORMATION: :
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LENGTH: 1361
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US-08-463-903-21
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APPLICANT: Affiniter, Joseph A.
APPLICANT: Affiniter, Joseph A.
APPLICANT: Affiniter, Joseph A.
APPLICANT: Affiniter, Joseph A.
APPLICANT: Kotite, Nicolas J.
TITLE OF INVENTION: Dimer and Multimer Forms of Single Chain Polypeptides
FILE REFREENCE: 40224A US
CURRENT APPLICATION NUMBER: US/07/935,695
CURRENT FILING DATE: 1992-08-21
PRIOR APPLICATION NUMBER: US 08/463,903
PRIOR FILING DATE: 1995-06-05
NUMBER OF SEQ ID NOS: 102
SOFTWARE: MS-Word for Windows, Ver. 7.0
SEQ ID NO 21
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                                                                                            GAATCCGGGGTCCCTGACCGATTCAGTGGCGGGCTCTGGGACAGATTTCACTCTCACC
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Pred. No. 6.2e-93;
0; Mismatches 18
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ORGANISM: Artificial Sequence
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ilarity 94.7%;
Conservative
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OTHER INFORMATION: :
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APPLICANT: Richard, Ruth A.
APPLICANT: Richard, Ruth A.
APPLICANT: Richard, Ruth A.
APPLICANT: Kotite, Nicolas J.
APPLICANT: No. Nicolas J.
APPLICANT: No. Nicolas J.
APPLICANT: NICOLAS J.
APPLICANT J.

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NAME/KEY: Human kappa subgroup IV VL (Hum4 VL) from pRL1001
US-07-935-695-3
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89.0%; Score 301.6; DB 3;

Best Local Similarity 94.3%; Pred. No. 1.6e-90;

Matches 313; Conservative 0; Mismatches 19;
CURRENT APPLICATION NUMBER: US/07/935,695
CURRENT FILING DATE: 1992-08-21
PRIOR APPLICATION NUMBER: US 08/463,903
PRIOR FILING DATE: 1995-06-05
NUMBER OF SEQ ID NOS: 102
SOFTWARE: MS-Word for Windows, Ver. 7.0
SEQ ID NO 3
LENGTH: 1088
TYPE: DNA
ORGANISM: HOMO Sapiens
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Patent No. 6071515
GENERAL INFORMATION:
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NAME/KEY: SCFV1 from pCGS515
LOCATION: 1..836
US-08-463-903-1
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US-08-463-903-1
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APPLICANT: Richard, Ruth A.
APPLICANT: Affolder, Joseph A.
APPLICANT: Affolder, Moseph A.
APPLICANT: Kotite, Nicolas J.
TITLE OF INVENTION: Dimer and Multimer Forms of Single Chain Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of Single Chain Polypeptides
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91.0%; Score 308.6; DB 3; Length 1088;
Best Local Similarity 94.4%; Pred. No. 8.9e-93;
Matches 320; Conservative 0; Mismatches 19; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: Human kappa subgroup IV VL (Hum4 VL) from pRL1001
1. LOCATION: 1..1088
US-08-465-903-3
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                                                                                                                                                                                                                                                                            RESULT 13
US-08-463-903-3
US-08-463-903-3
) Sequence 3, Application US/08463903
) Patent No. 6071515
(GENERAL INFORMATION:
) APPLICANT: Richard, Ruth A.
) APPLICANT: Richard, Ruth A.
) APPLICANT: Rocite, Nicolas J.
) TILLE OF INVENITON: Dimer and Multimer Forms of File Reference: 40224A US
) CURRENT APPLICATION NUMBER: US/08/463,903
) CURRENT FILING DATE: 1995-06-05
) EARLIER APPLICATION NUMBER: US 07/935,695
) RALIER APPLICATION NUMBER: US 07/935,695
) RALIER APPLICATION OFFICE O
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Sequence 3, Application US/07935695
Patent No. 6329507
GENERAL INFORMATION:
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                                                                                                                                              257 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGGGTCTGGGACAGATTTCACTCTCACC 316
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ALIGNMENTS

linear PRI 23-FEB-1993 chain variable	•	ı; Ig heavy		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 368)
linear r chain varia		nining regior region; IgM; sus.		/ertebrata; E Hominidae;
368 bp DNA A antibody heavy	igm line).	arity determ Ig variable s erythemato		Craniata; V Catarrhini;
368 anti-DNA an	(H)1 (III-2R	complement ght chain; stemic lupu		1; Chordata; 1; Primates; 3)
HSVH112RW 368 bp DNA linear PRI : H.sapiens DNA for anti-DNA antibody heavy chain variable	region, subgroup V(H)1 (III-2R IgM line). X70487 X63851 X70487.1 GI:38449	anti-DNA antibody; complementarity determining region; Ig heavy chain; Ig kappa light chain; Ig variable region; IgM; immunoglobulin; systemic lupus erythematoeus.	Homo sapiens. Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 368)
*		anti-E chain; immunc		
RESULT 1 HSVH112RM LOCUS DEFINITION	ACCESSION VERSION	KEYWORDS	SOURCE ORGANISM	REFERENCE

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/organism="Homo sapiens"
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/chromosome="14"
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/cell_type="B lymphocyte"
3730
/produce="ID"
/codon_start=1
/codon_start=1
/produce="ID"
/produce
IgG CLL buys-
receptors

AL Unpublished
CE 2 (bases 1 to 370)
)RS Chiorazzi,N.

B. Chiorazzi,N.

NAL Submitsed (02-SEP-1997) Medicine, North Shore University Hospital,
350 Community Drive, Manhasset, NY 11030, USA
Location/Qualiflars

1. 370

'`rqanism="Homo sapiens"
'`rqanism="Homo sapiens"
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428 bp mRNA linear PRI 08-MAY-2001
Homo sapiens clone 2lu-19 immunoglobulin heavy chain variable
region (IGH) mRNA, partial cds.
AF062105
AF062105.1 GI:3170672
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Homo sapiens ID:CLL008 IgM heavy chain variable region mRNA,
partial cds.
                                                                                                                                                                                                                     // Organism="Homo sapiens"
// Organism="Homo sapiens"
// Organism="Homo bli."
// Draganism="patient Dii."
// Draganism="patient Dii."
// Orione="patient Draganism="patient"
// Orione="Ib="genomic DNA in Charon 40"
// Orione="igM light chain variable region"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
(bases 1 to 370)
Chiorazzi,N.
Differences in Ig variable region gene use and mutation in IgM vs
         Manheimer-Lory, A., Katz, J.B., Pillinger, M., Ghossein, C., Smith, A. and Diamond, B.
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//note="complementarity determining region, CDR 1"

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/note="complementarity determining region, CDR 2"

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                                                          Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype J. Exp. Med. 174 (6), 1639-1652 (1991) 92078875 1660528
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| Godon_start=1
| product=1 | peavy chain"
| product=1 | d=1 AABO0781.1"
| db_xref="G1:185323"
| db_xref="GDB:G00-118-731"
| db_xref="GDB:G00-118-731"
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| GGTFSSYALSWVRQAPGGGLEWMGG1IPIFGTANYAQKFQGRVTITADESTSTAYMEL
| SSLRSEDTAVYYCAREGYCSSTSCSNWFDFWGQGTLVTVSS"
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                                                                                                                                                             (bases 1 to 525)

Kipps, T.J. and Duffy, S.F.
Relationship of the CD5 B cell to human tonsillar lymphocytes that express autoantibody-associated cross-reactive idiotypes
J. Clin. Invest. 87 (6), 2087-2096 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
                                                                                DNA
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                                                                            V-region; immunoglobulin heavy chain subgroup VH-I; rearranged DNJ Homo sapiens tonsil DNA. Homo sapiens Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Human Ig rearranged H chain gene V-region (V-D-J) hybridoma L22, subgroup VH-I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ų
                                                                                                                                                                                                                                                                                                                                                                                       /cell_type="B_lymphocytes"
/tissue_type="tonsil"
11. .525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="Ig heavy chain"
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/note="G00-118-731"
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/note:
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/gene="IGH@"
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/gene="IGH@"
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                                                               GI:185322
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         DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      /produčt="immunoglobulin heavy chain variable region"
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/db xref="GI:317673"
/translation="MDWTWRFLFVVAAATGVQSQVQLVQSGAEVKKPGSSVKVSCKAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGTFSSYAISWVRQAPQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMEL
SSLRSEDTAVYYCARDRVSGGSGYNWFDPGAREPWSPSPQG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 CCTGCAAGGTTCTGGAGGACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCC 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGGACAAGGGCTTGAGTGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
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                                                                           2 (bases 1 to 428)
Wang,X. and Stollar,B.D.
Direct Submission
Submitted (22-APR-1998) Biochemistry Department, Tufts University
School of Medicine, 136 Harrison Ave., Boston, MA 02111, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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     Immunoglobulin VH gene expression in human aging Clin. Immunol. 93 (2), 132-142 (1999) 99459182
                                                                                                                                                                                                                                                                                                  Cell type="peripheral B lymphocyte"/tissue_type="blood"/note="from elderly repertoire 21u"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 311.2; DB 9
Pred. No. 2.3e-84;
0; Mismatches 28
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                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromcome="14"
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/clone="21u-19"
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                                                                                                                                                                                                                                                                                                                                                                                                                                       codon_start=1
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/gene="IGH"
58.
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Best Local Similarity 92.1%;
Matches 339; Conservative
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/gene="IGH"
. 107 c
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/gene="IGH"
                                                                                                                                                                                                                                                                                                                                                                                                                   gene="IGH"
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TCTCCTCA 425
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gene="WH-69"
join(I. .46,133 .>512)
gene="WH-69"
join(I. .46,133 .>512)
gene="WH-69"
foodon start=1
foodon star
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homosapiens isolate HOW IgM heavy chain VH1 region precursor (VH1-59) gene, partial cds. U84173.1 GI:2344939
                                                                                                                                                                                 241 TGGAGCTGAGCCTGAGATCTGAGGACACGCCCTGTATTACTGTGCGAGAGATCCCG 300
                                                                                                                                                                                                                                                                                                   301 ATTATGTTTGGGGGAGGACAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGGTCATCG 360
350 CAATGACTACGGGGAGAGGGGGGACTACTGGGGAACTGGTGACTGGTCACG 418
359 CCAATGACTACGGGGGGGGGGGGACTACTGGGGCCAAGGGAACCTGGTCACG 418
179 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCAŢCCCTATCTTTGGTACAGCAAACTACG 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota, Metazoa; Chordata; Cararhini; Hominidae; Homo.
I (Dases 1 to 512)
Johnson, T. A., Rassenti, L. Z. and Kipps, T. J.
Ig Will genes expressed in B cell chronic lymphocytic leukemia exhibit distinctive solecular features
J. Immunol. 158 (1), 235-246 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (Dases 1 to 512)
Johnson, T. A.
Submitted (D8-JAM-1997) Medicine, UCSD, 9500 Gilman Drive, 0663,
Jolla, CA 92093, USA
1. .512
                                                                                                181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGGCGGACAAATCCACGAGCACAGCCTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 512;
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| Abolace="patient HOW" |
| Ab xref="taxon:9606" |
| Chromosome="14" |
| Map="1492" |
| /mote="CLL: chronic lymphocytic leukemia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             product="IgM heavy chain VH1 region"
/note="FW1/CDR1/FW2/CDR2/FW3/CDR3/FW4"
128 c 159 g 112 t
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/gene="VH1-69"
144. .512
/gene="VH1-69"
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                                                                                                                                                                                                                                                                                                                                                                                                                          361 TCTCCTCA 368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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H.sapiens mRNA for immunoglobulin heavy chain V-region (clone
CDN3IBS).
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                                                                                                              118
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                                    395 TGGAGCTGAGCCTGAGATCTGAGGACACGGCCCTGTACTGTGCGAGAGAGGAT 454
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Homuroglobulin; immunoglobulin heavy chain; variable region.

Homo sapiens.

Bunos sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Homanalia; Euthoria; Primates; Catarrhini; Hominidae; Homo.

1 (bases I to 113)

Demaison, C., David, D.; Letourneur, F., Zouali, M., Saragosti, S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT
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/db_xxef="kexon:9906"
/clone="CDNJ188"
/cll type="B-lymphocyte"
/tissue_type="peripheral blood lymphocyte"
/dev_stage="adult"
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/product="immunoglobulin variable region"
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515 CCGTCTCCTCA 525
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הטטטייים S21 bp DNA linear PRI 27-AUG-1997
Homo sapiens isolate LID IgM heavy chain VH1 region precursor
(VHI-69) gene, partial cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    360
                                                                                                                         CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
                                                                                                                                               CCTGCAAGGCTTCTGGAGGCACCTTCAGCACCTATGCTATCAGCTGGGGTGCGACAGGCCC 264
                                                                                                                                                                                                                                                                              CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
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                                                                                     145 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGAAGAAGAGCCTGGGTCCTCGGTGAAGGTCT 204
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Johnson, T.A.
Direct Subsasion
Submitted (008-JAM-1997) Medicine, UCSD, 9500 Gilman Drive, 0663,
Jolla, CA 92093, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTATGTTTGGGGGAGCGACAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGCTCATCG
                                                                                                                                                                                                                             CTGGACAAGGGCTTGAGTGGATGGAGGGATCATCCCTATCTTTGGAACAGCAAACCACG
                                                   AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGTCCTCGGTAAAGGTCT
           Gaps
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/producie=1gM heavy chain VH1 region precursor"
/protein_id="AACS1707.1"
/db_xref="GI:2344954"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/isolate="patient LiD"
/db_xref="taxon:9606"
/db_xref="14"
/map="11492"
/note="CLL: chronic lymphocytic leukemia"
             Indels
           38;
             Mismatches
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/gene="VH1-69"
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             Conservative
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B. (Dases 1 to 515)

B. Alklos, J.A. and Swerdlow, S.H.
Ongoing Ig Gene Hypermutation by Salivary Gland Mucosa-Associated Lymphold Tissue-Type Lymphomas

L. Blood (1997) In press

E. 2 (bases 1 to 515)

S. Bahler, D.W., Miklos, J.A. and Swerdlow, S.H.
Direct Submission

L. Submitted (26-NOV-1996) Pathology, Montefiore University Hospital, 200 Lothrop Street, Pittsburgh, PA 15213-2582, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSU79581 515 bp DNA linear PRI 01-FEB-1997
Human clone OR immunoglobulin heavy chain gene, partial cds.
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GGTFSTYAISWVRQAPGQGLEWMGGIIPIFGTANHAQKFQGRVTITADESTSTAYMEL
SSLRSEDTAVYYCAREGYDSSGSPKPFDYWGQGTLVTVSSG"
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                                                                                                                                           CCTGCAAGGCTTCTGGAGGCACCTTCAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
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protein_id="AAB41736.1"
db_xref="GI:1813666"
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Pred. No. 3.9e-83;
                             38;
         89.7%; Pred. No. 3.9e-83; ive 0; Mismatches 38
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="14"
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89.7%;
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                             330; Conservative
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Best Local S
Matches 330
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/partial
/gene="Id@"
/codon start=1
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/product="Ig heavy chain"
/brotania(="HAAA9225.1"
/db_xref="GI:185345"
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join(11. .56,143. .153)
/note="G00-118-731"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     387 bp mRNA linear PRI 08-WAY-2001
Homosapiens clone 48u-22 immunoglobulin heavy chain variable
AF062189.1 GI:3170840
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             294
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Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     215 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCC
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83.0%; Score 305.6; DB 9;
Best Local Similarity 90.6%; Pred. No. 1.2e-82;
Matches 339; Conservative 0; Mismatches 29;
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                                                                                                                                                                                                                                                                                                                                  /gene="IGH@"
/note="G000118-731"
143. -528
/gene="IGH@"
/product="Ig heavy chain"
/note="G00-118-731"
a 131 c 170 g 119 t
                                                                                                                                                                                                                                            /11.56
/gene="IGH@"
/product="Ig heavy chain"
/note="G00-118-731"
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Homo sapiens
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 387)
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Human Ig rearranged H chain gene V-region (V-D-J) hybridoma L42,
subgroup VH-I.

M65104. GI:185344
N M65104. GI:185344
N W65104. I GI:185344
NOW sapiens tonsil DNA.
NISM Homo sapiens Eucheria; Primates; Carariata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Cararrhini; Hominidae; Homo.

(CE 1 (Dases I to 528)
RSS Felationship of the CD5 B cell to human tonsillar lymphocytes that express autoantibody-associated cross-reactive idiotypes
AD J. Clin. Invest. 87 (6), 2087-2096 (1991)

NE 1710233
GGTFSSYAISWVRQAPGGGLEWMGRIIPILGIANYAQKFQGRVTITADKSTSTAYMEL
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/product="IgM heavy chain VH1 region"
/notes="Fw1/CDR1/Fw2/CDR2/Fw3/CDR2/Fw3/CDR3/Fw4"
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                                                                                                                                                                                                                                                                                                                                                                          CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCC 264
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                                                                                                                                                                                                                                                                                1 AGGTGCAGCTGCTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT
                                                                                                                                                                                                           DB 9; Length 521;
                                                                                                                                                                                                       Query Match 83.1%; Score 305.8; DB 9; Length Best Local Similarity 90.5%; Pred. No. 1.1e-82; Matches 341; Conservative 0; Mismatches 27; Indels
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1. .58
1. .58
| organism="Homo sapiens" |
| db_xref="taxon:9606" |
| map="14473.33" |
| fissue_type="bupphocytes" |
| 11. .528 |
| join(11. .56,143. .528)
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19 WH genes expressed in B cell chronic lymphocytic leukemia exhibit distinctive molecular features J. Immunol. 158 (1), 235-246 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CACAGAAGTICCAGGGCAGAGTCACGAITACCGCGGACGAAITCCACGAGCACAGCCTACA 384
                                                                                                                                                                                                                                                                          Johnston, T.A.
Direct Submission
Submitted (08-JAN-1997) Medicine, UCSD, 9500 Gilman Drive, 0663,
Jolla, CA 92033, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AGGIGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
/producie=1gM heavy chain VH1 region precursor"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              /map="14q32"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="VH1-69"
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/note="FW1/CDR1/FW2/CDR2/FW3/FW4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note="Allele: variants 1,5"
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//isolate="patient LAN"
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/gene="VH1-69"
                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9606"
     (VH1-69) gene, partial cds.
U84178
                                                                                                                                                                                                                                                                                                                                                                                                                                                /chromosome="14"
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/gene="VH1-69"
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144. .515
                                       U84178.1 GI:2344949
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                                                                          Homo sapiens
                                                                                            Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tränslation="QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQG
LEWMGGIIPIFGTANYAQKFQGRVTITADKSTSTAYMELSSLRSEDTAVYYCARQADC
SGGSCYDIFPNWFDPWGQGTLVTVSSG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSU84178 515 bp DNA linear PRI 27-AUG-1997
Homo sapiens isolate LAN IgM heavy chain VH1 region precursor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGGACAAGGGCTTGAGTGGGATGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGGACAAGGGCTTGAGTGGGATGGGATCATCCCTATCTTTGGTACAGCAAACTACG 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                            /codom start=1
product="laununoglobulin heavy chain variable region"
protein id="AAC18225.1"
/db_xref="GI:3170841"
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                                                                                                                                             Department, Tufts Ur
., Boston, MA 02111,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 304.6; DB 9; Length Pred. No. 2.4e-82; 0; Mismatches 24; Indels
Whang, X. and Stollar, B.D. Immunoglobulin VH gene expression in human aging Clin. Immunol. 93 (2), 132-142 (1999)
                                                                                                                                                                                                                                                                                                  /cell_type="peripheral B lymphocyte"
/tissue type="blood"
/note="from elderly repertoire 48u"
/gene="IGH"
                                                                                   2 (bases 1 to 387)
Wang, X. and Stollar, B.D.
Submission
Submission
Submitted (22-APR-1998) Biochemistry Del
School of Medicine, 136 Harrison Ave., 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79
                                                                                                                                                                                            1. .387
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="114"
/map="14q32.33"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAACCCTGCTCATCGTCTCCTCA 368
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                                                                                                                                                                            Location/Qualifiers
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89.8%;
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/gene="IGH"
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                                                                          10527689
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Best Local
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/codon_start=1
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/product="immunoglobulin heavy chain variable region"
/protein_id="AAA18279.1"
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TGLNWFDPWGQGTLVTVSS"
                                                                                                                                                                                                                                                                                                                                                                                                                                            U00583 363 bp mRNA linear PRI 25-MAY-1994
Human immunoglobulin heavy chain variable region (clone Tmu60)
mRNA, partial cds.
U00583 U00583.1 GI:392755
                                                                                                    241
                                                            181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
                                                                                                                                                                                                                     Homo sapiens

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (Dases 1 to 363)

Huang, C. and Srollar, B.D.

Am ajority of 1g H chain cDNA of normal human adult blood

lymphocytes resembles cDNA for fetal 1g and natural autoantibodies
CTGGACAAGGGCTTGAGTGGATGGGAAGGATCCTTCCTTGGTATAGCAAACTACG 181
                                                                                                                                            297
                                                                                                                                                               242 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGCCGTGTATTACTGTGCGAGATGCCATA 301
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                                                                                    182 CACAGAAGTTCCAGGGCAGAGTCACGGATTACCGCGGACAAAATCCACGAGCACAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGA---GATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 363)
Stollar.ba.D.
Direct Submission
Submitted (10-404-193) Stollar B.D., Tufts University,
Biochemistry, 136 Harrison Ave., Boston, MA 02111, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 363;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="male"
/cell_type="B-lymphocyte"
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/clone_lib="Tmu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .363
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Tmu60"
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                                                                                                                                                                                                                                                                                                    358 TCGTCTC 364
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KEYWORDS
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U00583
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/gene="1CH"
<1. .>372
/gene="1GH"
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LBWWGRIIPILGIIANYAQKFOGRVTITAAKSTSTAYMELSSLRSEDTAVYYCARCHTY
XDFWSGYYEDYAGGGGLUTVUSS"
* 115 g 84 t
                                                                                                                                                                                         372 bp mRNA linear PRI 02-JUL-2002
Homosapiens IGH mRNA for immunoglobulin heavy chain VHDJ region,
Partial cds, clone:ya0037h.
AB067158
AB067158.1 GI:21670372
299 CCGATTATGTTTGGGGGAGCGACAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGGTCA 357
445 CGGGGAGTTATTGCATTGTGCATTCGACCCCTGGGGGAACCCAGGGAACCCTGGTCA 504
                                                                                                                                                                                                                                                                                                                                                                                                                                          Akahori, Y., Iba, Y., Morino, K., Shinohara, M., Hirono, Y., Kakita, M., Suzuki, K., Torii, H., Ukai, Y., Honda, T., Katsumi, H., Okada, J., Miura, K. and Kurosawa, Y.

Construction and characterization of antibody libraries: isolation of therapeutic human antibodies and application to functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAAGAAGAGCCTGGGTCCTCGGTAAAGGTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (25-JUL-2001) Yoshikazu Kurosawa, Institute for Submitted (25-JUL-2001) Yoshikazu Kurosawa, Institute for Comprehensive Medical Science, Fujita Health University, Immunology; Kutoskake-cho, Toycake, Aichi 470-1192, Japan (Email:Kurosawa@tujita-hu.ac.jp, Tel:81-562-93-9387) Please visit our web site URL:http://www.fujita-hu.ac.jp/immunity/.
                                                                                                                                                                                                                                                                                                                                          Homo sapiens cDNA to mRNA, clone_lib:AIMS4 clone:ya0037h.
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 303; DB 9; Length 37 Pred. No. 7.5e-82; 0; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="AIMS4"
/note="mixture of tissues:tonsils,
peripheral blood and bone marrow"
1. 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="ya0037h"
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Best Local Similarity 91.0%;
Matches 334; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 372)
                                                                          358 TCGTCTCCTCA 368
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505 CCGTCTCCTCA 515
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                                                                                                                                                                                                                                                                             ACCESSION
VERSION
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ال 27-AUG-1997 S18 bp DNA linear PRI 27-AUG-1997
Homo sapiens isolate CRA IgM heavy chain VH1 region precursor
(VH1-69) gene, partial cds.
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                                                                                                                                                                                                                                                                                                       180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          504
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( Dases I to 518)
Johnson, T.A., Rassenti, L.Z. and Kipps, T.J.

Ig VH1 genes expressed in B cell chronic lymphocytic leukemia exhibit distinctive molecular features

J. Immunol. 158 (1), 235-246 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 518)
Johnson, T.A.
Johnson, T.A.
Submitted (008-JAN-1997) Medicine, UCSD, 9500 Gilman Drive, 0663, Jolla, CA 92093, USA
                                                                                                                Gaps,
                                                                                                                                                                                                                                                                                                       121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG
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                                                                                                                                                                                                                                                      205 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAACTGGGTGCGACAGGCCC
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127 c 165 g 119 t
                                                                        Score 300.8; DB 9;
Pred. No. 3.6e-81;
); Mismatches 32;
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/organism="Homo sapiens"
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/gene="VH1-69"
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/gene="VH1-69"
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Homo sapiens isolate BRA IgM heavy chain VH1 region precursor
(VH1-69) gene, partial cds.
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Johnson, T.A.
Direct Submission
Submitted (08-JAN-1997) Medicine, UCSD, 9500 Gilman Drive, 0663, La
Jolla, CA 92093, USA
Location/Qualifiers
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1 (bases 1 to 518.

Johnson, T.A., Rassenti, L.Z. and Kipps, T.J.

Ig VH1 genes expressed in B cell chronic lymphocytic leukemia exhibit distinctive molecular features
J. Immunol. 158 (1), 235-246 (1997)
                                                                                                                                                                                                                                                        242 TGGAGCTGAGCCTGAGATCTGAGGACACGCTGTGTATTACTGTGCGAGA-----G
 CCTGCAAGGCTTCTGGAGGCACCTTCAGTATATACTATCAGCTGGGTGCGACAGGCCC
                                     62 ccriscaagscrircrissassaccaccrircascrariscraricadorissasriscassacce
                                                                            CTGGACAAGGGCTTGAGTGGGATGGAATCATGCCTATCCTTGGACTAGCAAATTACG
                                                                                                                                                   CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA
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/product="Igh" chark fyety chain VH1 region"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
En (Dases 1 to 477)

NIH-MCC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Lu Onpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Ling Hong/Nubin Laboratory

CDNA Library Preparation: Ling Hong/Nubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM1211 row: n column: 14

High quality sequence stop: 473.

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                         GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Note: Libs is a NIH_NGC Library."
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Humman.

Humman.

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Humber, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

In (bases 1 to 909)

In (Mac. noi.nih.gov)

National Institutes of Health, Mammalian Gene Collection (MGC)

Nopublished (1999)

Contact: Robert Strausperg, Ph.D.

Fissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.
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/color: this is a NIH-MGC Library 2 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       325 TGGAGCTGAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGTAAGAT 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG
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Bukaryota, Metazoa; 'Chordata, Craniata, Vertebrata, Euteleosto
Mammalia; Eutheria, Primates, Catarrhini; Hominidae; Homo.
1 (Dases 1 to 1012)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov m.http://image.llnl.gov m.column: 03
high quality sequence stop: 848.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 12; Length 909;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

80.8%; Score 297.4; DB 12;
Best Local Similarity 89.5%; Pred. No. 1.8e-73;
Matches 332; Conservative 0; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BF974633.1 GI:12341848
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AUTHORS
TITLE
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/organisme="Homo sapiens"

/db xref="taxon:9666"

/clone="IMAGE:5301349"

/clone=lib="IMAGE:5301349"

/clone=lib="NHH MGC 113"

/lab_host="DH10B (phage-resistant)"

/note="Organ: spleen; Vector: pOTB7; Site 1: Xho1; Site 2:
ECORI; CDNA made by oligo-dT priming. Directionally cloned
into BCORI/Xho1 sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGGAGATCCCG 300
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                                                                                                                                          E l'angelia de la company de l
                                                   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   107 AGGTCCACCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGAAGACCTGGGTCCTCAGTGAAGGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          287 CACAGAAGTICCAGGGIAGAGICACGAITAGIGCGGACGAAICCACGAGCACAGCTACA
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78.2%; Score 287.8; DB 14; Length 959;
Best Local Similarity 87.9%; Pred. No. 9.5e-71;
Matches 326; Conservative 0; Mismatches 42; Indels 3;
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Location/Qualifiers
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              SOURCE
ORGANISM
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ORIGIN
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BG754936
LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db xref="taxon:966"
/db xref="Taxon:966"
/clone="InxAGE=*34774"
/clone=lib="InxH MGC 48"
/tissue_type="primary B-cells from tonsils (cell line)"
/tissue_type="primary B-cells from tonsils (cell line)"
/tab_host="DH10B (phage-resistant)"
/not="Organ: B-cells, Vector: pOTB7; Site_1: XhOI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhOI sites using the following 5' adaptor: gGCACGAGG(6). Size-selected >SODbp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH MGC Library. " I others
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BQ706226
BG706226.1 GI:21845125
BS7.
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                                        Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC Clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lln.gov
Plate: LLCM1204 row: m column: 15
High quality sequence stop: 716.
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286 240 346

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EST 15-MAY-2001

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Contact: Robert Strausberg, Ph.D.

Email: capabs-remail.nih.gov
Tissue procurement: Louis M. Staudt, M.D., Ph.D.

Contact: Robert Strausberg, Ph.D.

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Tissue procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CONTA Library Arrayed Dy: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: WGC clone distribution information can be http://image.llnl.gov

Clone distribution: WGC clone distribution information can be http://image.llnl.gov

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: WGC clone distribution information can be http://image.llnl.gov

Location/Qualifiers

1. 878

Corganisms="Homo sapiens"

(Ab_arref="taxon:9606"

(Alone="InxAgges")

(Alone="Inx
                                                                                                                                                                                                                      BG758459 878 bp mRNA linear EST 15-MAY-2001
602712658F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4852934 5',
mRNA sequence.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 878)

Nath-MOC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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77.6%; Score 285.4; DB 12; Length
Best Local Similarity 89.2%; Pred. No. 4.3e-70;
Matches 331; Conservative 0; Mismatches 36; Indels
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                       445 ACCGTCTCCTCA
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/ Organism="Homo sapiens"
/ Organism="Homo sapiens"
/ Clone="INAGE:4852039"
/ Clone="Organ: B-cells; Vector: POTB7; Site_1: XhoI;
/ Note="Organ: B-cells; Vector: POTB7; Site_1: XhoI;
/ Note="Organ: B-cells; Vector: POTB7; Site_1: XhoI;
/ Note: Inage: In
                                                                                                                                                                                   Homo sapiens

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases to 903)

SNIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Emali: cgapbs-r@mail.inih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Innyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be http://imagel.llnl.gov

Plate: LLCM1665 row: n column: 08

High quality sequence stop: 813.

Location/Qualifiers
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602711631F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4852039 5', mRNA sequence.
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                                                                  BG754936
BG754936.1 GI:14065589
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/clone_lib="NIH MGC_113"
/lab_host="DH10B" (phage-resistant)"
/lab_host="DH10B" (phage-resistant)"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
BCORI; cDNA made by oligo-dT priming. Directionally cloned
into BCORI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
                                                                                                                                                                                                                                                                                                            DUSBL378
AGENCOURT_8642770 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6295574
5', mRNA sequence.
301 ATTAIGITIGGGGGAGGGACAACIGGITCGACCCCIGGGGCCAGGGAACCCIGCTCAICG 360
                                                      TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGGAGAGATCCCG 300
                                                                             342 TGGAGCTGAAACAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGTGGGGA 401
                                                                                                                                                              402 ACACACCICCTTGGTTTG---GTGTGTTTGACTACTGGGGCCAGGGAACCCTGGTCACCG 458
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Pred. No. 2.3e-69;
0; Mismatches 45;
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/clone="IMAGE:6295574"
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-340 c 276
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Best Local Similarity 87.1%;
Matches 323; Conservative 0
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                                                                                                                                                                                                    368
                                                                                                                                                                                                                                      459 TCTCCTCA 466
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AGENCOURT_8354485 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6281064
5', mRNA sequence.
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                                                        385 ATTGTAGTAGTACCAGCTGCCTGTACTTTGACTACTGGGGCCA-GGAACCCTGGTCA 443
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325 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGTAAGAT 384
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM243 row: e column: 01
High quality sequence stop: 576.
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                                       ATTATGTTTGGGGGGGGGGGCAC---AACTGGTTCGACCCCTGGGGCCAGGGAACCCTGCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AGGIGCAGCIGGIGCAGICTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .903
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:581064"
                                                                                                                                                                                                                                                                                                              BQ706171.1 GI:21845070
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Matches 323; Conservative
                                                                                                             358 TCGTCTCCTCA 368
                                                                                                                                             444 CCGTCTCCTCA 454
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_7977406 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6216047
                              240
      284 CTGGACAAGGCTTGAGTGGATGGAGGGATCATCCTATCTTTGCTACATCAAAGTACG 343
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                                                        TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
                                                                     404 redadcuearecercadarereadacacacecerararrarerecadadarecec 463
                           CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAACTACA
                                                                                    301 ATTATGTTTGG---GGGAGCGACAACTGGTTCGACCCCTGGGCCCAGGGAACCCTGCTCA
                                                                                                 464 GTATGGGTCGGGGAGGTATATCGGGCTGGTTCGACCCCTGGGGCCAGGGAACCCTGGTCA
                                                                                                                                                                                5', mRNA sequence.
BQ708591 GI:21847477
                                                                                                                  358 TCGTCTCCTCA 368
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1 ÀGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAGCCTGGGTCCTCGGTAAAGGTCT

Cth 78; Score 282:4; DB 14; Length 980; Al Similarity 87:8; Pred. No. 3:2e-69; 323; Conservative 0; Mismatches 36; Indels 9;

Query Maťch Best Local S Matches 323

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1. .991
| Organism="Mone sapiens"
| Organism="Mone sapiens" |
| Ab xref="taxon:9606" |
| Alone="IMAGE:6214702" |
| Alone="IMAGE:6214702" |
| Alone="IMAGE:6214702" |
| Alone="IMAGE:6214702" |
| Alone="Organ: Spleen; Vector: pOTB7; Site_1: XhoI; Site_2: BCORI; DNA made by olique-dr priming. Directionally cloned into EcoRI/XhoI sites using the following 5; adaptor: into EcoRI/XhoI sites using the following 5; adaptor: GGGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Matazoa, Chordata, Craniata, Vertebrata; Euteleostomi, Bukaryota, Matazoa, Chordata, Craniata, Vertebrata; Euteleostomi, I (Dases 1 to 991)

1 (Dases 1 to 991)

1 (Dases 1 to 991)

1 NH-MGC http://mgo.nci.nih.gov/.

1 National Institutes of Health, Mammalian Gene Collection (MGC)

1 Unpublished (1999)

1 Contact: Robert Strausberg, Ph.D.

2 Email: Gappba-remail.nih.gov

Tissue Procurement: Dr. Mark Watson

CONTACT: Robert Strausherg, Ph.D.

2 Contact: Robert Strausherg, Ph.D.

2 Contact: Robert Strausherg, Ph.D.

2 Contact: Robert Strausherg, Ph.D.

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2 Contact: Robert Strausherg, Ph.D.

2 Contact: Robert Strausherg, Ph.D.

2 Contact: Robert Strausherg, Ph.D.

3 Tissue Procurement: Dr. Mark Watson

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

4 High quality sequence stop: 587.

4 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGENCURT_1976230 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6214702 5', MRNA sequence.
BQ710257 BQ710257.1 GI:21849156
EST.
Homean.
Home sapiens
EVENTATION OF THE SET                                                                                                                                                                                                                                                     177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGCCTGGGTCCTCGGTGAAGGTCT
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BQ710257
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210

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AW408371 16-FEB-2000 UI-HF-BK0-abk-c-03-0-UI.rl NIH_MGC_36 Homo sapiens cDNA clone IMAGE:3056620 5', mRNA sequence.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 417)
NHH-MGC http://mgc.nci.nih.gov/.
NHH-MGC http://mgc.nci.nih.gov/.
Ontional Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGAGCTGAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-remail.nih.gov

Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M.B. Soares Lab

CDNA Library Arrayed by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www.bio.llnl.gov/bbrp/image/image.html

Seq primer: M13 Porward.
                                                                                                                                                                                                                                                                                                                                                                                                  CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC
                                                                                                                                                                                                                                                        AGGTGCAGCTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT
           this is
                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                     .,
3
Superscript II RT (Life Technologies). Note:
NIH MGC Library."
1 312 c 273 g 178 t 3 others
                                                                                                                                            Length 970;
                                                                                                                                         Score 279; DB 14; Length 9
Pred. No. 3e-68;
); Mismatches 45; Indels
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/cell_type="1ymph"
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AW408371.1 GI:6927428
                                                                                                                                            75.8%;
86.9%;
                                                                                                                                            Query Match
Best Local Similarity 86.9
Matches 319; Conservative
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BQ706539 68706539.1 GI:21845438
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/db_xref="taxon.9606"
/clone=lib="NHH MGE 113"
/lab_host="DH10B" (phage-resistant)"
/lab_host="DH10B" (phage-resistant)"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 970)

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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                 Gaps
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CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can k
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2515 row: c column: 23
High quality sequence stop: 569.
Location/Qualifiers
                                                              9
              DB 14; Length 991;
                                                              Indels
                                                                 44;
     76.5%; Score 281.6; DB 1.
ilarity 86.6%; Pred. No. 5.5e-69;
Conservative 0; Mismatches 44
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        355 TCATCGTCTCTCA 368
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                                     Similarity
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                                                         324;
     Query Match
Best Local S
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/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2: ECORI, COMPA made by oligo-dr priming. Directionally cloned into EcoRI/XhoI sites using the following 5 adaptor: GCACGAG(6). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Burkaley) using ZAP-cDNA synthesis kit (Stratagene) and NH_MGC Library in RT (Life Technologies). Note: this is a 291 c 246 g 162 t
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Bukaryota, Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Macazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

SEMANDA STANDA ST
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Pred. No. 9.1e-68;
0; Mismatches 43; Indels 6;
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                                                                                                                                                                                                                                                                                                                                                                                 75.3%;
86.7%;
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Best Local Similarity 86.79
Matches 319, Conservative
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/cell_line="MGC85"
| Ala host="HHIOB (LTI)"
| Alab host="HHIOB (LTI)"
| Alab host="Vectors | PT713-Brac; Site_1: NotI; Site_2: Eco RI;
| Constructed from size fractionaled cytoplasmic mRNA
| Constructed from size fractionally cloned.
| Constructed from Directorally cloned. Cells provided by Louis
| M. Staufsk, Ph.D. Library preparation by Maria de Fatima
| Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

I (bases 1 to 884)

I (bases 1 to 884)

NIH-MGC http://mgc.noi.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg; Ph.D.

Contact: Robert Strausberg; Ph.D.

Tissue Procurement: Dr. Mark Watson

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)

Clond Altribution: MGC clone distribution information can be http://image.llnl.gov.b. Goolwing. 24

High quality sequence stop: 631.

Licraniam="Homo sabiens"

Licraniam="Homo sabiens"
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BQ708380 BQ708380.1 GI:21847279
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75.8%; Score 278.8; DB 10; Length 417;
Best Local Similarity 88.5%; Pred. No. 2.2e-68;
Matches 317; Conservative 0; Mismatches 32; Indels 9;
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/lab_host="DH10B (phage-resistant)"
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/note="Wector: pr773-Pac, Site 1: Not1; Site 2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (0.5-1.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Benaido, Ph.D. and M. Bento Soares, Ph.D."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTTTCAGCTGGGTGCGACAGGCCC 134
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           at:
         Consortium/LLNL
                                                                                                                                                                                                                                      B cells"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 276.6; DB 10
Pred. No. 9.3e-68;
0; Mismatches 49
                                                                                               1. .418
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/cell_line="MGC85"
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www-bio.llnl.gov/bbrp/image/image.html
Seg primer: M13 Forward.
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ilarity 86.0%;
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/organism="Homo sapiens"

/db_xref="taxon:9606"
/clone="IMAGE:6215114"
/clone="IMAGE:6215114"
/clone="IMAGE:6215114"
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/note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2: EcoH1; cDNA made by oligo-dT priming. Directionally cloned into EcoMI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Garald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mamaalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 418)
S NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
L Onbublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbersremanil.nih.gov
ECORI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AW401468 418 bp mRNA linear EST 16-FEB-2000 UI-HF-BKO-aad-f-06-0-UI.rl NIH MGC_36 Homo sapiens cDNA clone IMAGE:3053339 5', mRNA sequence.
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Scoring table:

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ABL65479
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AAX05452
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619..972
7.tag= b
11361..1465
7.tag= c
1154..1883
7.tag= d
11950..2273
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/*tag=
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Human HIV-1 monocl
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                                                                                                                                            July 18, 2003, 04:14:58; Search time 95.4001 Seconds (without alignments) 8686.944 Million cell updates/sec
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| SIDSZ/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
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                 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
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AAA48411
AAF29714
AAQ22419
AAQ44185
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Gapop 10.0 , Gapext 1.0
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Score

Result No.

DNA encoding anti-Human FVIII antibo Human secreted pro

Anti-FAPalpha ant: Human anti-GPIIb/:

Humanised murine

Human secreted pro CEA6 antibody sing DNA encoding anti-Anti-human CD154 a

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CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
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         extravasation-dependent adverse reaction; organ damage; clotting; adult respiratory distress syndrome; glomerular nephritis; ischaemic myocardial injury; immune reaction; septic shock; septicaemia; therapy; diagnosis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79.7%; Score 293.2; DB 18; Length 2287; 88.2%; Pred. No. 5.6e-75; ive 0; Mismatches 33; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                          P-selectin and opt. E-selectin binding organic mol. - having sialyl-Le(x) and sulphated determinant, useful for protecting against inflammatory or immune reactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2287 BP; 483 A; 758 C; 648 G; 398 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 40-41; 81pp; English.
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hes 335; Conservative
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P-PSDB; AAW10550.
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                                                                                            Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 134 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAATGCTATCAGCTGGGTGCGACAGGCCC
                                                                                                                                                                                                                                               The IgG1, in its nascent form, bears no sialyl-Lex side chains. The inventors designed a molecule including several such sites for attachment of sialyl-Lex side chains (see AAR2442, FT). The additional N-linked glycosylation sites are introduced at locations which impair complement fixing and Fr seceptor binding ability. They are preferably located in the CHZ region of the Ig molecule. Antibodies bearing multiple sialyl-Lex determinants are useful for disrupting undesirable interactions between cells or proteins. Bisrupting this interaction has therapeutic applications, for example, in minimising inflammation following tissue injury.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79.7%; Score 293.2; DB 13; Length 2287; ilarity 88.2%; Pred. No. 5.6e-75; Conservative 0; Mismatches 33; Indels 12;
                                                                                                                                                 Inhibition of cell adhesion mediated through ELAM-1 mol. bindi
- used in treating chronic inflammation, rheumatoid arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IgG1; P-selectin ligand; PSGL-1; counter-receptor; E-selectin; sialyl-Lewis X; antiinflammatory; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2287 BP; 483 A; 753 C; 652 G; 399 T; 0 other;
                                                                                                                                                                                                                   Disclosure, Fig 1, 46pp, English.
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90US-0618314
                                 (GEHO ) GEN HOSPITAL CORP
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P-PSDB; AAR24442.
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Best Local Similarity
Matches 335; Conserv
                                                                  Walz G;
                                                                                                                                                                                    psoriasis, etc.
 23-NOV-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides the protein and coding sequences for the variable regions of human monoclonal antibodies which are immunoreactive with human immunodeficiency virus-1 (HTV-1) envelope glycoprotein gpl20. These can be used in diagnosis and therapy of HIV-1 infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human monoclonal antibody immunoreactive with human immunodeficiency virus-1 glycoprotein gpl20, useful for detecting HIV-1 in biological sample and providing passive immunotherapy to HIV-1 infected mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT
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                                                                                                                                                                                                                                                                                                                                                  Human immunodeficiency virus-1; HIV-1; human monoclonal antibody; envelope glycoprotein; gpl20; diagnosis; ds.
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                                                                                                                                                                                                                                                                                   Human HIV-1 monoclonal antibody coding sequence SEQ ID NO: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 378 BP; 81 A; 93 C; 122 G; 82 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78.7%; Score 289.6; DB 2; 88.0%; Pred. No. 3.9e-74; ive 0; Mismatches 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (USSH ) US DEPT HEALTH & HUMAN SERVICES.
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                                                                                       AAF29080 standard; DNA; 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-JUN-2000; 2000WO-US17327.
                                                                                                                                                                                                                   (first entry)
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Matches 329; Conservative
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P-PSDB; AAB62779.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                                      AAF29080
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                                                     AAF29080
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CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence encodes a recombinant human antibody scFv. Antibody TN11 reacts with the long form of human Tenascin-C (TN-C). The epitope recognised by TN11 is located inside domain C of TN-C. TN11 is therefore only capable of recognising TN-C isoforms containing domain C (cTN-C). TN11 is useful for detecting the presence of TN-C isoforms in vitro or in vivo for diagnosing pathologies expressing the cTN-C isoforms of TN-C. It is useful for the preparation of formulations for the treatment of human neoplasias.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGGACAAGGGCTTGAGTGGATGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGCCGTGTATTACTGTGCGAGAGATCCCG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; antibody scFv; TN11; Tenascin-C; TN-C; domain C-containing TNC;
cTN-C; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGGTGCTGGTGCAGTCTGGGCTGAGGTGAAGAAGCCTGGGTCTCGGTGAAGGTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ligands used for diagnosis and treatment of human neoplasias, are capable of identifying the tenascin-C isoform containing domain {\tt C}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51; Indels
                                                                                                                                                                                                                                                                                                                                                                Recombinant human antibody scFv TN11 nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 747 BP; 157 A; 197 C; 231 G; 162 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 286.4; DB 2:
Pred. No. 3.9e-73;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 8; Page 5-6; 31pp; English.
                                                                                                                                                                                          BP.
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86.1%;
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Matches 317; Conservative
355 TCATCGTCTCCTCA
                                                                                                                                                                                          AAC67868 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PHIL-) PHILOGEN SRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                         16-FEB-2001
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The present sequence encodes the heavy chain variable region of a human tumour-specific monoclonal antibody. Meoplastic cells selectively express antigodies can be produced that are specifically directed against tumour-specific antigens. The antibodies can be conjugated to cytoctoxic or cytostatic agents and used to selectively target cancer cells for the confidence of tumours. They can also be linked to diagnostic moieties that allow the imaging of neoplastic cells. Nucleic acids encoding human tumour-specific monoclonal antibodies can be used to express the antibodies with higher affinity or higher selectivity for tumour cells. The unclosed were produced by hybridomas that were generated by in vitro immunisation of human spleen cell cultures with breast carcinoma cells. The nucleic acid encoding the monoclonal antibody encoding the monoclonal antibody encoding the monoclonal antibody encoding the monoclonal antibody encoding the monoclonal antibody encoding the human monoclonal antibody encoding the region which was produced by LHI3 hybridoma cell line.
ATTATGTTTGGGGGAGCGACAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGCTCATCG 360
                                                                             GTATTACGATTTTTGGAGGAGGTGCTTTCGATATCTGGGGCCGAGGCATGTTTTTGGAGGTCACCG 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New tumor-specific human monoclonal antibody, useful for the treatment and diagnosis of cancer, comprises at least one complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product= "LH13 antibody heavy chain variable region"
                                                                                                                                                                                                                                                                                                                                                  Human; LH13 monoclonal antibody; hybridoma; tumour-specific; cancer; cytostatic; cytotoxic; heavy chain variable region; ss.
                                                                                                                                                                                                                                                                                                                   Human LH13 monoclonal antibody heavy chain variable region cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 16; Page 82; 84pp; English.
                                                                                                                                                                                                                         AAA48411 standard; cDNA; 354 BP.
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P-PSDB; AAY99558.
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Sequence 3,54 BP; 80 A; 90 C; 115 G; 69 T; 0 other;

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CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
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                                                                                                                                                                                                                                                                    182 CACAGAAGTICCAGGGCAGAGTCACGATTACCGCGGACGAATCCACGAGCACAGCCTACA 241
                                                                                                                                                                                                                                                                                                                            242 TGGAGCTGAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGGGAGA---- 296
                                                                                                                                                                                                                                                                                                                                                                                         -----AGATAGCAGTGGCTGGTATCACTACTGGGGCCAGGGAACCCTGGTCACCG
                                                               9
                                                                                                                                                                                                                                                                                                    241 TGGAGCTGAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention provides a composition comprising a homodimeric immunoconjugate protein made up of two chains, each containing an IgG1 Fc effector domain and a targeting domain. The targeting domain may be
                                                                                          61
                                                                                                                                                                             121 CTGGACAAGGGCTTGAGTGGATGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG
                                                                                                                                                                                                         122 CTGGACAAGGGCTTGAGTGGATGGAGGGATCATCCTATCTTTGGTACAGCAAACTACG
                                                          1 AGGIGCAGCIGGIGCAGICIGGGGCIGAGGIGAAGAAGCCIGGGICCICGGIAAAAGGICI
                                                                                        AGGTGCAGCTGCAGTCTGGGGCTGAGGTGAAGAGCCTGGGTCCTCGGTGAAGGTCT
                                                                                                                                                 62 ccrecaagecricigaagecaccricageageciarecrarcageriegeriegacagecee
                                                                                                                                                                                                                                       181 CACAGAAGTICCAGGGCAGAGICACGATTACCGCGGACAAAICCACGAGCACAGCCTACA
                                                                                                                                                                                                                                                                                                                                                              301 ATTATGTTTGGGGGGGGGGGGACAACTGGTTCGACCCCTGGGGGCCAGGGAACCCTGCTCATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunoconjugate protein for treatment of neovascularization, comprises protein comprising Fc region of human immunoglobulin (1g)GI conjugated to the targeting domain which comprises factor VII mutant -
                                 Gaps
                                 15;
Score 284.8; DB 21; Length 354;
Pred. No. 9.5e-73;
); Mismatches 27; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse; scFv; immunoconjugate; 1gG1 effector domain; catherosclerosis; tissue factor; macular degeneration; rheumatoid arthritis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G71-1 immunoconjugate coding sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAF29714 standard; DNA; 1517 BP.
Query Match 77.4%;
Best Local Similarity 88.6%;
Matches 326; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                          TCTCCTCA 368
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91WO-US06185
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Best Local Similarity 96.0
Matches 288; Conservative
                                                                   (GENP-) GENPHARM INT INC
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P-PSDB; AAR22358.
                                                                                                                                                                              human placental
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                       28-AUG-1991;
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29-AUG-1990;
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      19-MAR-1992
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    VII. The
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              factor.
                                                                                                                                                               either term of human 1gG1 Fc region or a mutant form of human factor VII. immunoconjugate is targeted at the transmembrane receptor tissue factor This enables the composition to be used in the treatment of diseases associated with neovascularisation, including cancer, atherosclerosis,
                                                                                                               1 AGGTGCAGCTGCAGTCTGGGGCTGAGGTGAAGACCCTGGGTCCTCGGTAAAGGTCT
                                                                                                                                AGGTGCAGCTGGTGCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT
                                                                                                                                                   CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC
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                                                                           DB 22; Length
                                                                                              32; Indels
                                                         Sequence 1517 BP; 338 A; 444 C; 441 G; 294 T; 0 other;
                                                                          Score 282.8; DB 2
Pred. No. 5.2e-72;
); Mismatches 32
                                         rheumatoid arthritis and macular degeneration.
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88.0%;
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/*tag= a
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                                                                                              Matches 324; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vector lambda FIX II was screened with the human VH1 family specific oligonucleotide (see AAQ22418). Phage clone lambda 49.8 was isolated and a 6.1 kb Xbal fragment contg. the variable segment VH49.8 subcloned into pNN03 to generate plasmid pVH49.8 An 800 bp region of this insert was sequenced. VH49.8 was found to have an open reading frame and intect splicing and recombination seignals, thus indicating that the gene is functional.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genomic DNA library cloned into the phage
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Pred. No. 1.7e-71;
0; Mismatches 12;
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isotype switching; H chain variable region;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 14; Page 87; 172pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers 1..286
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96.0%;
90US-0575962.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ44185 standard; DNA; 812
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us-09-627-896b-29.rng

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CTGGACAAGGGCTTGAGTGGATGGAAGGATCATGCTATCCTTGGACTAGCAATTACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      445 CCTGCAAGGCTTCTGGAGGCACCTTCAGCTATGCTATCAGCTGGGTGCGACAGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AGGIGCAGCIGGIGCAGICTGGGGCTGAGGTGAAGAAGCCTGGGTCTCGGTAAAGGICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         385 AddrccAdcrdGrdcAgrcrdGddcrdAddAddAddccrdGdrcrcGdrcAAGGrcr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is the variable heavy chain gene segment containing human DNA fragment, vh49.8 which was injected into half day mouse embryo pronuclei, to generate an unrearranged heavy chain minilocus transgene. The resulting transgenic mice can be used for the production of heterologous (i.e. human) antibodies against specific antigens, this comprises immunising a mouse with a preselected antigen and collecting antigen binding heterologous human gamma immunoglobulins.
                                                                                                                                                                                                         Variable; heavy chain; gene segment; human; DNA fragment; vh49.8; unrearranged; minilocus; transgene; transgenic; mouse; production; heterologous; antibody; gamma; immunoglobulin; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76.3%; Score 280.8; DB 17; Length 812; 96.0%; Pred: No. 1.7e-71; ive 0; Mismatches 12; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of heterologous human immunoglobulin(s) - by immunising
                                                                                                                                                                          DNA fragment vh49.8, containing variable heavy chain gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 812 BP; 204 A; 188 C; 223 G; 197 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 12; Columns 61-62; 94pp; English.
                                                                                                                                                                                                                                                                                                            Location/Qualifiers
241.286
/*tag= a
373.437
/*tag= b
                                                                            AAT37243 standard; DNA; 812 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92US-0990860.
90US-0574748.
90US-0575962.
91US-08130279.
92US-0853408.
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                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 76.3
Best Local Similarity 96.0
Matches 288; Conservative
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P-PSDB; AAW03950.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kay RM, Lonberg N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transgenic mice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-DEC-1992;
29-AUG-1990;
31-AUG-1990;
17-DEC-1991;
18-MAR-1992;
23-JUN-1992;
                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                             21-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-AUG-1990;
                                                                                                                                                                                                                                                                                                                                                                                                            US5545806-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                             13-AUG-1.996
                                                                                                             AAT37243;
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                                             RESULT 9
                                                                                           DP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGGACAAGGGCTTGAGTGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        564
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGGACAAGGGCTTGAGTGGGAAGGATCATCCTATCCTTGGTATAGCAACTACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            385 AGGICCAGCIGGIGCAGICTGGGCTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              445 ¢cidcaAddctrcrgaAddcaccrrcaGcaGcrargcrarcaGcrgaGdGcGACAGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAAGCCTACA
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/*tag= ~ // humber= 1
287..372
/*tag= b
// number= 1
373..812
// tag= c
// number= 2
241..689
// *tag= d
// note= "CDS is interrupted by intron #1; the last three codons of the CDS are not translated in the amino acid sequence AAR38623"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A human placental genomic DNA library cloned into the phage vector lambda FIX II was screened with the human VH1 family specific oligonucleotide AAQ44184. Phage clone lambda 49.8 was isolated and 6.1kb Xbal fragment containing the variable segment VH49.8 was subcloned into pNNO3 to generate plasmid pVH49.8. An 800bp region of this insert was sequenced (AAQ44185) and VH49.8 found to have an open reading frame and intact splicing and recombination signals, indicating that the gene is functional.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 76.3%; Score 280.8; DB 14; Length 812; Best Local Similarity 96.0%; Pred. No. 1.7e-71; Matches 288; Conservative 0; Mismatches 12; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 812 BP; 204 A; 188 C; 223 G; 197 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                              91US-0810279.
92US-0853408.
92US-0904068.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1993-214169/26.
P-PSDB; AAR38623.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kay RM, Lonberg N;
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18-MAR-1992;
23-JUN-1992;
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switching in lymphocytes
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                                                                                                                                                                                                                                                                                                                                                                Transgenic mouse; human; immunoglobulin; heavy chain segment; J region; joining region; constant region; VH family; variable gene; gamma isotype; diversity gene; isotype switching sequence; mu isotype; Ig production; monoclonal antibody; MAD production; antigen; heavy chain isotype;
                                                                      624
                                                                                                 CACAGAAGTICCAGGGCAGAGTCACGAITACCGCGGACAAAICCACGAGCACAGCCIACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human antibody producing transgenic mouse - containing transgene comprising human V, D and J genes and sequences to provide isotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= a
/note= "contains an intron, no stop codon given"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
241..678
                                                                                                                                                                                                                          AAV12538 standard; DNA; 812 BP
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90US-0574748.
90US-0575962.
91US-0810279.
92US-0853408.
92US-0990860.
93US-0953131.
                                                                                                                                                                                                                                                                                                                              Human VHI family gene VH49.8.
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93US-0161739.
93US-0165699.
94US-0209741.
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373..678
/*tag= d
/number= 2
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/*tag= c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-DEC-1994;
                                                                                                                                                                                                                                                                                             26-MAY-1998
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                                                                  565
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contains in its genome a transgence comprising in operable linkage human variable (V), diversity (D) and junction (J) genes, a human mu constant region gene (muCH), at least 2 different non-um human CH genes and secolated isotype switching sequences, where human mu and gamma switch sequences are located in closer proximity to each other than in the naturally occurring human immunoglobulin (Ig) locus, and where in lymphocytes of the mouse the transgene undergoes productive VDJ rearrangement and mu to gamma isotype switching by recombination between the human mu and gamma sequences, so that the mouse produces a serum containing Ig of at least 3 human heavy chain isotypes in response to antigenic stimulation. The transgenic mice can be used to produce human clipming climble in the transgenic mice can be used to produce human antigens. The MAD can be used in therapeutic or diagnostic applications. The transgenic mice can produce human MAD of multiple isotypes by undergoing isotype switching.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240
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                                                              This sequence represents the human VHI family gene VH49.8. This DNA sequence can be used in a plasmid, which is used to develop the transgenic mouse of the invention. The transgenic mouse of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGACACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          385 AGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                445 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAATTACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    565 cacagaagirccaggggagagrcacgarraccgggacaaarccacgagcacagcrraca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunoglobulin heavy chain, variable region, V region, VH1 family, transgene, monoclonal antibody; heterologous antibody; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 18; Length 812;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 1.7e-71;
0; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 812 BP; 204 A; 188 C; 223 G; 197 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag=_a
Product= VH49.8
/note= "heavy chain V region gene"
287..372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 280.8;
Example 12; Column 73-74; 153pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAT70522 standard; DNA; 812 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76.3%;
96.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-MAR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 96.09
Watches 288; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241..677
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transgene;

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/*tag= c
/number= 2
/note= "The protein shown in the specification ends at
position 677, not at the stop codon ending at
position 689"
                                                                                                                                                                DNA sequence in the specification is unclear, so this is the best estimate of the sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel anti-CD4 antibody produced by transgenic mice - used in the treatment of auto-immune disease etc.
            Ig; affinity constant; human; antigen; hybridoma; B cell; tr
transgenic; mouse; CD4; antibody; autoimmune; inflammatory;
transplant rejection; immunoglobulin; ss.
                                                                                 Location/Qualifiers
241..286
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/*articodon= 1
/note= "DNA se
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                                                                                                                                                                                                                                                                                                                 96WO-US16433.
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'number= 1
                                                                                                                                                                                     373..812
                                                                                                                                                                                                                                                                                                                                                         (GENP-) GENPHARM INT INC.
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P-PSDB; AAW24777.
                                                                                                                                                                                                                                                                                                                                                                                 Lonberg
                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                              10-OCT-1996;
                                                                                                                                                                                                                                                                  WO9713852-A1
                                                                                                                                                                                                                                                                                       17-APR-1997.
                                                                                                                                                                                                                                                                                                                                      10-OCT-1995;
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                                                                                                                                                                                      exon
                                                                                Key
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                                                                                                                                                                                                                                                                                                                      This sequence encodes the VH49.8 gene from the human heavy chain V region and a member of the VH1 family. This gene was sequenced from the plasmid pVH49.8 which is used in a novel method of developing transgenic non-human animals capable of producing heterologues antibodise encoded by human immunoglobulin genes. Such transgenically produced monoclomal antibodies should alleviate the intrinsic immunogenicity of non-human immunoglobulins allowing the development of new in vivo applications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          385 AGGICCAGCIGGIGCACTCIGGGGCTGAGGTGAAGAAGCCTGGGICCTCGGTCTAAGGTCT 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     445 CCTGCAAGGCTTCTGGAGGCACCTTCAGCTATGCTATCAGCTGGGTGCGACAGGCCC 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGGACAAGGGCTTGAGTGGGAAGGATCATGCTAATCCTTGGACTAGCAAATTACG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAATCCACGAGCACAGCCTACA 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   505 CTGGACAAGGGCTTGAGTGGATGGAATCATCCCTATCCTTGGTATAGCAAACTACG 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGGAGCTGAGGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CACAGAAGITCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                 Transgenic mouse for heterologous antibody production - containing DNA encoding human immunoglobulin components
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 76.3%; Score 280.8; DB 18; Length 812; Best Local Similarity 96.0%; Pred. No. 1.7e-71; Matches 288; Conservative 0; Mismatches 12; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 812 BP; 204 A; 188 C; 223 G; 197 T; 0 other;
 /*tag= c /*tag= c /*tag= c /*tag= c /*tag= c /*tag= c /*tag= c /*tag= mentioned in specification" /*tag= "Mentioned in specification"
                                                                                                                                                                                                                                                                                                   Example 14; Column 54; 90pp; English
                                                                                                                                                   90US-0574448.
                                                                                                                               92US-0834539
                                                                                                                                                                                                                              WPI; 1997-297410/27.
N-PSDB; AAW18840; AAW18841.
                                                                                                                                                                                    (GENP-) GENPHARM INT INC.
                                                                                                                                                                                                           Lonberg N;
    misc_feature
                                    misc_feature
                                                                                                                           05-FEB-1992;
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31-AUG-1990;
                                                                                US5633425-A
                                                                                                     27-MAY-1997
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                                  A novel composition has been developed which comprises an immunoglobulin [1g] having an affinity constant (Ra) of at least 2 multiply 10000000000 M-1 for binding to a predetermined human antigen. The present sequence represents the human VH1 gene VH49.8 isolated from a human placental genomic library lambda. Anti-CD4 antibodies from may be used in therapeutic and diagnostic applications, especially activity of CD4 cells and reduce undesirable autoimmune reactions, inflammatory response and remosplant rejection. Transgenic animals are capable of producing heterologous antibodies of multiple isotypes by is necessary for antigen-stimulated B-cell maturation and can give that encode and produce nor more subsequent heterologous isotypes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                445 ccidcaadgcircingaagcaccircagcaactarcararcagciagarccacacagc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGGACAAGGGCTTGAGTGGATGGAAGGATCATGCCTATCGTTGGACTAGCAATTACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                DB 18; Length 812;
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 76.3%; Score 280.8; DB 18; Length Best Local Similarity 96.0%; Pred. No. 1.7e-71; Matches 288; Conservative 0; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                    Sequence 812 BP; 203 A; 194 C; 223 G; 192 T; 0 other;
Example 12; Page 138; 396pp; English.
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AAT73471 standard; DNA; 812

Human VH1 gene VH49.8.

23-JAK-1998

AAT73471;

CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The specification describes transgenic animals that are capable of producing a heterologous antibody. The antibodies are isolated form a hybridoma, comprising B cells, that is obtained from a transgenic mouse having a genome comprising a human heavy chain transgene and a human light chain transgene. The B cells are fused to immortalized cells amount of an immunoglobulin that specifically binds digoxin or shinga-like toxin. B cells from transgenic animals can be used to generate hybridomas expressing monoclonal high affinity human sequence antibodies produced from the transgenic animals of the invention can be used to treat human diseases, e.g. autoimmune diseases, cancer, infectious diseases, transplant rejection, blood disorders such as coagulation disorders and other diseases.
                 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA
                                                                TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG
                                                                                                                                                                                                                                                                                                              Transgenic animal, heterologous antibody; hybridoma, B cell; transgenic mouse; human heavy chain transgene; digoxin; human light chain transgene; immortalized cell; immunoglobulin; Shinga-like toxin; autoimmune disease; cancer; infectious disease; transplant rejection; blood disorder; coagulation disorder; 8s.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          present sequence represents human heavy chain V region gene VH49.8, which is used in the course of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transgenic non-human animals used to produce heterologous
                                                                                                                                                                                                                                                                                 Nucleotide sequence of human heavy chain V region gene VH49.8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 812 BP; 204 A; 188 C; 223 G; 196 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 12; Page 168; 484pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ball WJ;
                                                                                                                                                                                  BP.
                                                                                                                                                                                AAZ21897 standard; DNA; 812
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                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GENP-) GENPHARM INT INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9945962-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-MAR-1998;
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                                                                                                                                                                                                                 AAZ21897;
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                                  504
                                                                      180
                                                                                                        564
                                                                                                                                            240
                                                                                                                                                                                624
                                                                                                                                                                                                                                        TGGAGCTGAGCCTGAGATCTGAGGACACGCCGTGTATTACTGTGCGAGAGACACAG 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, Immunoglobulin transgene; Ig; VH gene; D gene; JH gene; mu gene; switch sequence; gamma gene; IgM; IgG; ss.
                                                                                                    505 CTGGACAAGGGCTTGAGTGGATGGGATCATCCCTATCCTTGGTATAGCAAACTACG
                                                                                                                                                                  445 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCC
                                                                                                                                            CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA
                                                                                                                                                                                                                   TGGAGCTGAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG
                                                                       CTGGACAAGGGCTTGAGTGGAATGGAATCATGCCTATCCTTGGACTAGCAAATTACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a heavy chain (human) immunoglobulin (Ig) transgene. The transgene comprises: (i) human VH gene segments; (ii) human D gene segments; (iii) human JH gene segments; and either (iv) in unan U gene segments; and either (iv) in unan U gene segments; and either (iv) in constant region comprising a mu switch sequence upstream from a mu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human immunoglobulin transgene - with mu and gamma isotype switching
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence of human VH1 family gene VH 49.8.
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                                                                                                                                                                                                                                                                                                                                              BP
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90US-0574748.
90US-0575962.
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97US-0800353.
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                                                                                                                                                                                                                                                                                                                                                                                                                      10-MAY-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                  AAX06042;
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12; Indels

· 0; Mismatches 76.3%; Score 280.8; 96.0%; Pred. No. 1.7

Matches 288; Conservative

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Local Similarity

Query Match

1.7e-71

DB 20; Length 812;

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animals to produce heterologous (human) Ig's with varying specificities. The presence of mu and gamma switch segments allows isotype switching of the human heavy chain mini-locus from IgM (for maturation) to IgG.
                                                                                                                         1 AGGICCAGCIGGIGCAGICTGGGGCTGAGGAGAAGCCTGGGTCTCGGTAAAGGTCT
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                                                                        Query Match 76.3%; Score 280.8; DB 20; Length 812; Best Local Similarity 96.0%; Pred. No. 1.7e-71; Matches 288; Conservative 0; Mismatches 12; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       daves ophthalmopathy associated immunoglobulin protein; orbital antigen; monoclonal antibody; heavy chain; H chain; variable region; VH; autoimmunity; ss.
                                                Sequence '812 BP; 204 A; 188 C; 223 G; 197 T; 0 other;
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P-PSDB; AAR72069.
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                                                                                      1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT
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                                           75.7%; Score 278.6; DB 16; Length 294; 96.9%; Pred. No. 5.6e-71; ive 0; Mismatches 9; Indels 0;
                       94 G; 57 T; 0 other;
                   Sequence 294 BP; 69 A; 74 C;
                                                      Best Local Similarity 96.9
Matches 284; Conservative
OF7H1.2, are provided.
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| cgn2_6/prodata/1/pubpna/USO6_NEW_PUB.seq:*
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Sequence 41, Appl
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US-10-166-23-35

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US-10-29-774-669-1

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CTGGACAAGGGCTTGAGTGGGATGGATCATGCCTATCCTTGGACTAGCAAATTACG 180 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCC 1 AGGIGCAGCIGGIGCAGICIGGGGCIGAGGIGAAGAGCCIGGGICCICGGIAAAGGICI CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC Gaps 7; DB 10; Length 495; Sequence 9.2 Application US/09925299; Patent No. US20020055627A1; GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: ROSEN et al.; TITLE OF INVENTION: Mucleic Acids, Proteins and Antibodies FILE REFERENCE: PA102; CURRENT FILING DATE: 2001-08-10; PRIOR PAPLICATION NUMBER: PCT/US00/05883; PRIOR FILING DATE: 2001-08-10; PRIOR FILING DATE: 2000-03-08; PRIOR FILING DATE: 1999-03-12; NUMBER OF SEQ ID NOS: 1556; SOFTWARE: Patentin Ver. 2.0; SEQ ID NO 92; LENGTH: 495 Indels Query Match 75.4%; Score 277.6; DB 10; Best Local Similarity 85.7%; Pred. No. 3.3e-84; Matches 318; Conservative 3; Mismatches 43;) OTHER INFORMATION: n equals a,t,g, or c US-09-925-299-92 FEATURE:
NAME/KEY: misc feature
LOCATION: (402) TYPE: DNA ORGANISM: Homo sapiens

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; OTHER INFORMATION: DNA encoding A010D09 scFv
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                                                                                                                                                                                                                                                                                                                                       Sequence 92, Application US/09925299
| Publication No. US20030040617A9
| Publication No. US20030040617A9
| GENERAL INFORMATION:
| APPLICANT: Rosen et al.
| APPLICANT: Rosen et al.
| TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
| FILE REFERENCE: PAIO2
| CURRENT APPLICATION NUMBER: US/09/925,299
| CURRENT FILING DATE: 2001-08-10
| PRIOR FILING DATE: 2000-03-08
| PRIOR PILING DATE: 1999-03-12
| NUMBER OF SEQ ID NOS: 1556
| SOFTWARE: Patentin Ver. 2:0
| SEQ ID NO 92
| LENGTH: 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
SGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
COCATION: (402)
COCATION: (402)
US-09-925-299-92
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US-09-925-299-92
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RESULT 4
US-10-091-300-19
US-10-091-300-19
Sequence 19, Application US/10091300
Publication No. US20030108545A1
GENERAL INFORMATION:
APPLICANT: Rockwell, Patricia
APPLICANT: Rockwell, Patricia
TITLE OF INVENTION: Combination Methods of Inhibiting Tumor Growth With a Vascular
FILE REFERENCE: 11245/46211 Growth Factor Receptor Antagonist
CURRENT APPLICANTON NUMBER: US/10/091,300
CURRENT FILING DATE: 2002-03-04
NS-10-151-882-9

1 Sequence 9, Application US/10151882

2 Sequence 9 Application US/10151882

3 Sequence 9. Application WS/20030059862A1

3 GENERAL INFORMATION:

4 APPLICATION NO Antibodies Against Tumor Necrosis Factor Delta (APRIL)

5 FILE REFERENCE: PFS54

6 CURRENT PELING DATE: 2002-05-22

7 FRIOR APPLICATION NUMBER: 05/293,100

8 RIOR APPLICATION NUMBER: 60/293,100

9 RIOR APPLICATION NUMBER: 60/293,100

9 SEQ ID NOS: 48

9 SOFTWARE: PatentIn version 3.0

1 LENGTH: 723

1 TYPE: DNA

1 ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 75.2%; Score 276.8; DB 15; Length 723; Best Local Similarity 87.2%; Pred. No. 6.8e-84; Matches 321; Conservative 0; Mismatches 32; Indels 15; Gaps
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TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cancer TITLE OF INVENTION: Sets

TITLE OF INVENTION: Sets

FILE REPRENCE: 68220-76

CURRENT APPLICATION NUMBER: US/09/954,456

CURRENT FILING DATE: 2001-09-18

PRIOR APPLICATION NUMBER: US/60/234,052

PRIOR APPLICATION NUMBER: US/60/234,923

PRIOR FILING DATE: 2000-09-26

PRIOR APPLICATION NUMBER: US/60/235,134

PRIOR FILING DATE: 2000-09-25

PRIOR APPLICATION NUMBER: US/60/235,134

PRIOR FILING DATE: 2000-09-25

PRIOR APPLICATION NUMBER: US/60/235,637

PRIOR FILING DATE: 2000-09-26

PRIOR FILING DATE: 2000-09-26

PRIOR FILING DATE: 2000-09-26

PRIOR APPLICATION NUMBER: US/60/235,637

PRIOR FILING DATE: 2000-09-26

PRIOR APPLICATION NUMBER: US/60/235,638

PRIOR FILING DATE: 2000-09-26

PRIOR APPLICATION NUMBER: US/60/235,638
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                                                                                                                                                                                            Length 1599;
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                                                                                                                                                                                         Score 274; DB 11;
Pred. No. 7.5e-83;
0; Mismatches 45;
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PRIOR FILING DATE: 2000-09-27
PRIOR PELLOATION NUMBER: US/60/235,720
PRIOR PELLOATION NUMBER: US/60/235,840
PRIOR FILING DATE: 2000-09-27
PRIOR PELLING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              349 CCCTGCTCATCGTCTCCTCA 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCCTGGTCACGTCTCCTCA 472
  SCFTWARE: PatentIn version 3.0 SEQ ID NO 789 LENGTH: 1599 TYPE: DNA TYPE: DNA ORGANIEM: Homo sapiens US-09-954-456-789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                            74.5%;
ilarity 85.0%;
Conservative
                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                            Query Match
Best Local Simi
Matches 323;
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TITLE OF INVENTION: Sets.

TITLE OF INVENTION: Sets.

TITLE OF INVENTION: Sets.

CURRENT APPLICATION NUMBER: US/09/954,456

CURRENT APPLICATION NUMBER: US/00/233,617

PRIOR PELING DATE: 2000-09-18

PRIOR APPLICATION NUMBER: US/60/234,052

PRIOR APPLICATION NUMBER: US/60/234,923

PRIOR PILING DATE: 2000-09-25

PRIOR PELING DATE: 2000-09-25

PRIOR PELING DATE: 2000-09-26

PRIOR PLING DATE: 2000-09-26

PRIOR PLING DATE: 2000-09-26

PRIOR PLING DATE: 2000-09-26

PRIOR APPLICATION NUMBER: US/60/235,637

PRIOR PLING DATE: 2000-09-26

PRIOR PLING DATE: 2000-09-26

PRIOR PLING DATE: 2000-09-26

PRIOR PLING DATE: 2000-09-26

PRIOR PLING DATE: 2000-09-26

PRIOR PLING DATE: 2000-09-26

PRIOR PLING DATE: 2000-09-26

PRIOR PLING DATE: 2000-09-26

PRIOR PLING DATE: 2000-09-26

PRIOR PLING DATE: 2000-09-26

PRIOR PLING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: US/60/235,710

PRIOR PLING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: US/60/235,940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
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                                                                                                                                                                                                                                                                             Gaps
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9
                                                                                                                                                                                                                     Length 375;
                                                                                                                                                                                                                                                                          45; Indels
                                                                                                                                                                                                                     Score 276; DB 15;
Pred. No. 1.1e-83;
                                                                                                                                                                                                                                                                          0; Mismatches
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FILING DATE: 2000-09-27
APPLICATION NUMBER: US/60/235,840
FILING DATE: 2000-09-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/60/235,863
FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 85
SOFTWARE WardPerfect 8.0 for Windows
SEQ ID NO 19
LENGTH: 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 789, Application US/09954456
Patent No. US20020115057A1
GENERAL INFORMATION:
                                                                                                                                                                                                                     75.0%;
86.2%;
                                                                                                                                                                                                                                                                       Matches 319; Conservative
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                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                          ; TYPE: DNA
; ORGANISM: Human
US-10-091-300-19
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US-09-954-456-789
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US SEQUENCE 46, Application US/10047542

SEQUENCE 46, Application NO. US2020168367A1

SERBEAL INFORMATION:
APPLICANT: LARRICK, JAMES W.
APPLICANT: LARRICK JAMES W.
TITLE OF INVENTION: AND BACTERIAL DISEASES
TITLE OF INVENTION: AND BACTERIAL DISEASES
FILE REFERENCE: 030905.0004.CIP1
CURRENT RELING DATE: 2001-10-26
PRIOR APPLICATION NUMBER: PCT/US01/13932
PRIOR APPLICATION NUMBER: PCT/US01/13932
PRIOR APPLICATION NUMBER: 60/200,298
PRIOR APPLICATION NUMBER: 60/200,298
PRIOR APPLICATION NUMBER: 60/200,428
PRIOR APPLICATION NUMBER: 0201-04-28
PRIOR PRIOR PRIOR SEQ ID NOS: 101
SOFTWARE: PATENTE 100 NO 46
LENGTH: 213
TYPE: DNA
CRANISM: Homo sapiens
US-10-047-542-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            311 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCCACGAGCACAGCCTACA 370
                                                                                                                                         181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCTACA 240
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               CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCC 178
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; Sequence 3, Application US/10151882
; Sequence 4, Application US/10151882
; GENERAL INFORMATION
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL); CURRENT APPLICATION NUMBER: US/10/151,882
                                                                                             CTGGACAAGGGCTTGAGTGGATGGGATCATCCTTTGGTACAGCAAACTACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   131 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCTCGGTGAAGGTCT
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11 TGGAGCTGAGCACCTGAGATCTGAGGACACGGCCGTGATTACTGTGCGAAA 423
371 TGGAGCTGAGCTGAGCTGAGGACACGGCCGTGATTACTGTGCGAAA 423
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Pred. No. 3.4e-82;
0; Mismatches 13;
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Best Local Similarity 95.6%;
Matches 280; Conservative
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Sequence 61, Application US/10047542

Publication No. US2020168367A1

GENERAL INFORMATION:

APPLICANT: LARRICK, JAMES W

APPLICANT: LARRICK, JAMES W

TITLE OF INVENTION: NOVEL INVUNDADHESINS FOR TREATING AND PREVENTING VIRAL

TITLE OF INVENTION: NOWBER: US/10/047,542

CURRENT APPLICATION NUMBER: US/10/047,542

CURRENT FILING DATE: 2001-10-26

FRIOR APPLICATION NUMBER: PCT/US01/13932

PRIOR FILING DATE: 2001-04-28

PRIOR APPLICATION NUMBER: 60/200,298

PRIOR APPLICATION NUMBER: 60/200,298

NUMBER OF SEQ ID NOS: 101

SEQ OF WARE PATENTIN VET: 2.1
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74.0%; Score 272.2; DB 15; Length 1884;
Best Local Similarity 95.6%; Pred. No. 3.2e-82;
Matches 280; Conservative 0; Mismatches 13; Indels 0;
                                                                                                                                      Length 1599;
                                                                                                                                         Query Match 74.5%; Score 274; DB 11; 1 Best Local Similarity 85.0%; Pred. No. 7.5e-83; Matches 323; Conservative 0; Mismatches 45;
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                                 . LENGTH: 1599
TYPE: DNA
. ORGANISM: Homo sapiens
US-09-954-456-1604
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TYPE: DNA
CRGANISM: Homo sapiens
US-10-047-542-61
SEQ ID NO 1604
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   CTGGACAAGGGCTTGAGTGGATGGAAGGATCATCCCTATCTTTGGTACAGCAACTACG 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 12, Application US/09811737; Patent No. US20020099180A1; Patent No. US20020099180A1; GENERAL INFORMATION; APPLICANT: Bochringer Ingelheim Pharma KG; TITLE OF INVENTION: Human FAP-alpha-specific antibodies; FILE REFREENCE: 1-1129; CURRENT APPLICATION UNMBER: US/09/811,737; CURRENT APPLICATION UNMBER: 2001-03-19; NUMBER OF SEQ ID NOS: 32; SOFTWARE: Patentin Ver. 2.1; SEQ ID NO 12; LENGTH: 396
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US-09-811-737-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     · 0; Mismatches
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Matches 312; Conservative
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Sequence 10, Application US/10151882

Sequence 10, Application US/10151882

Publication No. US20030059862A1

GENERAL INFORMATION:
TITLE OF INVENTYON: Antibodies Against Tumor Necrosis Factor Delta (APRIL)

FILE REFERENCE: PF554

CURRENT APPLICATION NUMBER: US/10/151,882

CURRENT APPLICATION NUMBER: 60/293,100

PRIOR APPLICATION NUMBER: 60/293,100

PRIOR PILING DATE: 2001-05-24

NUMBER OF SEQ ID NOS: 48

SOFTWARE: Patentin Version 3.0

LENGTH: 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCTGCAAGGCTTCTGGAGGCACCTTCAGTAATACTATCAGCTGGGTGCGACAGGCCC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             72.8%; Score 268; DB 15; Length 735; 94.9%; Pred. No. 6.6e-81; ive 0; Mismatches 15; Indels
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85.9%; Pred. No. 9e-81;
ive 0; Mismatches 34; Indels
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US-10-151-882-10
                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: DNA encoding A004G02 scFv
US-10-151-882-3
CURRENT FILING DATE: 2002-05-22 PRIOR APPLICATION NUMBER: 60/293, PRIOR FILING DATE: 2001-05-24 NUMBER OF SEQ ID NOS: 48 SOFTWARE: Patentin version 3.0 SEQ ID NO 3
                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
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Matches 277; Conservative
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Best Local Similarity 85.9
Matches 316; Conservative
                                                                                                                                                                                                                  LENGTH: 735
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US-10-151-182-11

ys-10-151-182-11

y Sequence 11, Application US/10151882

y Bublication No. US2003065862A1

y GENERAL INFORMATION:
    TILE NEPROMATION:
    TILE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)

y FILE REPREMENCE: PF554

CURRENT APPLICATION NUMBER: US/10/151,882

CURRENT APPLICATION NUMBER: 60/293,100

PRIOR APPLICATION NUMBER: 60/293,100

PRIOR APPLICATION NUMBER: 60/293,100

NUMBER OF FEO ID NOS: 48

SOFTWARE: PatentIn version 3.0

SEQ ID NO 11

LENGTH: 717

TYPE: DNA

ORGANISM: Artificial Sequence
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RESULT 12
US-09-811-737-22
Sequence 22, Application US/09811737
Sequence 22, Application US/09811737
Sequence 22, Application US/09811737
Sequence 22, Application US/09811737
Sequence 22, Application US/09811737
SUREMAL PROMATION: Human FAP-alpha-specific antibodies
FILE REFERENCE: 1-1129
CURRENT FILING DATE: 2001-03-19
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 22
TANGER 1782
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                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
J. OTHER INFORMATION: Humanised Antibody
US-09-811-37-27-8
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Publication No US20030059862A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVERTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
TITLE OF INVERTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
CURRENT APPLICATION NUMBER: US/10/151,882
CURRENT FILING DATE: 2002-05-22
PRIOR PRIOR PELICATION NUMBER: 60/293,100
PRIOR FILING DATE: 2001-05-24
SEQ ID NOS: 48
SOFTWARE: Patentin Version 3.0
SEQ ID NO SEQ ID NOS: 48
TENGTH: 744
TYPE: DNA
TYPE: DNA
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                                                                                                                                         1 AGGIGCAGCTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT
                                                                                                                                                                          2 AGTACAGCTGCAGCAGTCAGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT
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                                                                   Query Match 71.6%; Score 263.6; DB 15; Length 717; DB 15 best Local Similarity 93.5%; Pred. No. 2.1e-79; Matches 275; Conservative 0; Mismatches 19; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 71.6%; Score 263.6; DB 15; Length 744; Best Local Similarity 93.5%; Pred. No. 2.1e-79; Matches 275; Conservative 0; Mismatches 19; Indels 0;
; FEATURE:
-1 OTHER INFORMATION: DNA encoding A027H08 scFv
US-10-151-882-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; FEATURE:
- OTHER 18.P-7
US-10-151-882-7
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US-10-151-882-7
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RESULT 15
US-10-151-882-5
is Sequence 5, Application US/10151882
is Sequence 5, Application No. US20030059862A1
is GENERAL INFORMATION:
is APPLICANT: Ruben, Steven M.
if TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
is FILE REFERENCE: PFS54
is CURRENT APPLICATION NUMBER: US/10/151,882
is CURRENT FILING DATE: 2002-05-22
is PRIOR FILING DATE: 2001-05-24
is NUMBER OF SEQ ID NOS: 48
is SOFTWARE: PatentIn version 3.0
is SEQ ID NO 5
is LENGTH: 744
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242 IGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTCTATTACTGTGCGAGAG 295
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Pred. No. 3.9e-79;
0; Mismatches 42; Indels 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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71.4%;
Best Local Similarity 85.2%;
Matches 310; Conservative
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Search completed: July 18, 2003, 15:38:40 Job time : 89.9613 secs THIS PAGE BLANK (USPTO)

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1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
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Matches 335; Conservative 0; Mismatches 33; Indels
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Sequence 1, Appli
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Sequence 8, Appli
                                                                                  July 18, 2003, 09:26:19; Search time 19:5137 Seconds (without alignments) 5783.490 Million cell updates/sec
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368
1 aggtgcagctggtgcagtct......ccctgctcatcgtctcctca 368
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(cgn2_6/ptodata/1/ina/5A_COMB.seq:*

(cgn2_6/ptodata/1/ina/5A_COMB.seq:*

(cgn2_6/ptodata/1/ina/6A_COMB.seq:*

(cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*

(cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*

(cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-652-816A-44
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US-08-08-533-231
US-08-08-417A-79
US-08-053-131-61
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US-09-611-451-43
US-08-591-632-51
US-08-217-918-3
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Maximum Match 100%
Listing first 45 summaries
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Sequence 1, Applia Sequence 1, Applia Sequence 1, Applia Sequence 8, Applia Sequence 18, Applia Sequence 16, Applia Sequence 2, Applia Sequence 85		Length 2287;
28 248 67.4 687 5 05-05-95-11-25-11-	RESULT 1 US-08-480-036-1 IS-08-480-036-1 Sequence 1, Application US/08480036 Patent No. 572383 Fabrent No. 572383 Fabrent No. 572383 FITTE OF INVENTION: INHIBITION OF CELL ADHESION TITLE OF INVENTION: INTERACTIONS FITTE OF INVENTION: INTERACTIONS FITTE OF INVENTION: INTERACTIONS FORRESPONDENCE ADDRESS: 4 CORRESPONDENCE ADDRESS: 4 CORRESPONDENCE FISH & Richardson STREET: 225 Franklin Street CITY: Boston STREET: 225 Franklin Street CITY: Boston STREET: 255 Franklin Street CITY: Boston STREET: 255 Franklin Street CITY: Boston STREET: 255 Franklin Street COMPUTER: 180 PS/2 Model 50Z or 55SX OWNUTER: 180 PS/2 Model 50Z or 55SX OFFWARE: 180 PS/2 Model 50Z or 55SX OFFWARE: 180 PS/2 Model 50Z or 55SX OFFWARE: 180 PS/2 Model 50Z or 55SX OFFWARE: 180 PS/2 Model 50Z or 55SX OFFWARE: 180 PS/2 Model 50Z or 55SX OFFWARE: 180 PS/2 Model 50Z or 55SX OFFWARE: 180 PS/2 Model 50Z or 55SX OFFWARE: 180 PS/2 Model 50Z or 55SX OFFWARE: 180 PS/2 Model 50Z or 55SX OFFWARE: 180 PS/2 Model 50Z or 55SX OFFWARE: 180 PS/2 Model 50Z or 55SX OFFWARE: 180 PS/2 Model 50Z or 55SX OFFWARE: 180 PS/2 Model 50Z or 55SX OFFWARE: 180 PS/2 Model 50Z or 55SX OFFWARE: 180 PS/2 Model 50Z or 55SX OFFWARE: 180 PS/2 Model 50Z or 55SX OFFWARE: 180 PS/2 Model 50Z or 55SX OFFWARE: 180 PS/2 Model 50Z or 55SX OFFWARE: 180 PS/2 OR 57235838mber 23, 1990 TELEPROMY: 180 PS/2 OR 57235838mber 23, 1990 TELEPROMY: 180 PS/2 OR 572 OR	Query Best

1;

12; Gaps

120

240

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121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCÀAATTACG 180
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Sequence 1, Application US/08462571

Sequence 1, Application US/08462571

Sequence 1, Application US/08462571

Sequence 1, Application US/08462571

Sequence 1, Application US/08462571

Setent No. 5896983

TITLE OF INVENTION: Brian et al.

TITLE OF INVENTION: BROTEIN-CARBOHYDRATE INTERACTIONS

NUMBER OF SEQUENCES: S

CORRESPONDENCE ADDRESS:

STREE: ADSECONINGES: S

COUNTRY: US.A.

STREE: Massachusetts

COUNTRY: US.A.

COUNTRY: US.A.

CONPUTER: IBM PS.C. DOS (Version 3.30)

COMPUTER: IBM PS.C. DOS (Version 5.0)

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM PS.C. DOS (Version 5.0)

CURRATING SYSTEM: IBM PC. DOS (Version 3.30)

SOFTWARE: Wordberfect (Version 5.0)

CURRENT APPLICATION NUMBER: US/08/462,571

FILING DATE: 0.5 June 1995

CLASSIFICATION NUMBER: 03.238

REGISTRATION NUMBER: 35.238

REGISTRATION NUMBER: 35.238

REGISTRATION NUMBER: 35.238

REGISTRATION NUMBER: 35.238

REGISTRATION INFORMATION:

TELECOMMUNICATION INFORMATION
     Pred. No. 7.4e-83;
0; Mismatches 33; Indels
88.2%;
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TELEFAX: (617) 542-8906
Best Local Similarity 88.2
Matches 335; Conservative
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
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TITLE OF INVENTION: INHIBITION OF CELL ADHESION
TITLE OF INVENTION: INHIBITION OF CELL ADHESION
TITLE OF INVENTION: INHIBITION OF CELL ADHESION
TITLE OF INVENTION: PROTEIN-CARBOHYDRATE INTERACTIONS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADBRESS:
ADDRESSEE: 125 Franklin Street
CITY: Boston
STATE: MA
COUNTY: USA
ZIP: MA
COUNTY: USA
ZIP: O210-2804
COMPUTER READABLE FORM:
WEDIUM TYPE: PLORPY disk
COMPUTER: EIM PC Compatible
COMPUTER: EIM PC Compatible
COMPUTER: BATENION PATA:
MEDIUM TYPE: O5-UOS/MS-DOS
SOFTWARE: Datentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 07/618,314
FILING DATE: 05-UNM-1995
CLASSIFICATION NUMBER: US 07/618,314
FILING DATE: 23-NOV-1990
ATTORNEY/AGENT INPORMATION:
REGISTRATION NUMBER: 05-UNM-1995
REFERENCE/BOCKET NUMBER: 07786/667003
TELECOMMONICATION INFORMATION:
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Patent No. 5801044
GENERAL INFORMATION:
APPLICANT: Seed et al., Brian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTCCTCA 368
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
LENGTH: 2287
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STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                   1 AGGIGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGACTTGGGTCCTCGGTAAAGGTCT
                                                                                               Gaps
                                                                                             12;
                                                           DB 2; Length 2287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8, Application PC/TUS9610043
GENERAL INFORMATION:
APPLICANT: The General Hospital Corporation
TITLE OF INVENTION: P-SELECTIN LIGANDS AND RELATED MOLECULES
TITLE OF INVENTION: AND METHODS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS: 14
                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUFTWARE: Patentin Release #1.0, Version #1.30. CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10043
                                                         Score 293.2; DB 2;
Pred. No. 7.4e-83;
0; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  00786/284001
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,213
FILING DATE: 14-JUN-1995
CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 02210-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                       Query Match
Best Local Similarity 88.2%;
Matches 335; Conservative
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NAME: Lech, Karen F.
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER:
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TELEX: 200154
INFORMATION FOR SEQ ID NO:
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STREET: 220
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US-08-462-571-1
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APPLICANT: Allen, DJ
APPLICANT: Allen, DJ
APPLICANT: McCafferty, JG
TITLE OF INVENTION: Specific binding members, materials and
TITLE OF INVENTION: methods.
NUMBER OF SEQUENCES. 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COMPUTER: Illinois
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBP PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
CORRENT APPLICATION DATA:
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Pred. No. 7.4e-83;
0; Mismatches 33
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23-MAY-1996
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.8
FILING DATE: 02-DEC-1991
PRIOR APPLICATION DATA:
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                                                                                                                                                                                       TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

PCT-US96-10043-8
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SEQUENCE CHARACTERISTICS:
LENGTH: 2287 base pain
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity
Matches 335; Conservat
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CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
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                                                                                                         CORRESPEDENCE ADDRESS:

CORRESPONDENCE ADDRESSE:

ADDRESSEE:

Marchall, O'TCOle, Gerstein, Murray & Borun STRET:

CIT! Chicago

STATE:

Lilinois

COMPUTRY:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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             TITLE OF INVENTION: methods.
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 312-474-6300 IFORMATION FOR SEQ ID NO: 4 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAACTCTCCTATCAACTGGCTGCGACAGGCCC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182 CTCAGAAGTTCCAGGGCAGACTCACGATTACCGCGGACGAATCCACGCGCACAGCCTACA 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          242 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGTGCGAGACATAATC 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AGGIGCAGCTGGTGCAGTCTGGGGGCTGAGGTGAAGAAAAAAGGTCCTCGGTAAAGGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 AGGTTCAGCTGCTTCAGTCTGGGGCTGAGGTGAAGACCTTGGGTCCTCGGTGAAGGTCT
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Best Local Similarity 86.0%; Pred. No. 9.48-80;
Matches 313, Conservative 0; Mismatches 51; Indels 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5-08-652-816A-44
Sequence 44, Application US/08652816A
Sequence 47, Application US/08652816A
Sequence 48, Application US/08652816A
Settle APPLICANT: Osbourn, JK
APPLICANT: Allen, DJ
APPLICANT: McCafferty, JG
TITLE OF INVENTION: Specific binding members, materials and
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24 MAR-1992
APPLICATION DATA: 1992
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 23 SEP-1992
FILING DATE: 0.23 SEP-1992
FILING DATE: 0.25 SEP-1995
FILING DATE: 0.7 DEC-1995
FILING DATE: 0.7 DEC-1995
FILING DATE: 0.7 DEC-1995
FILING DATE: 0.2 MAY-1996
FILING DATE: 0.2 DEC-1992
APPLICATION NUMBER: GB 9610824.6
FILING DATE: 0.2 DEC-1992
PRIOR APPLICATION DATA: 0.8 96414,597
FILING DATE: 0.2 DEC-1992
FILING DATE: 0.2 DEC-1993
APPLICATION NUMBER: US 08/244,597
FILING DATE: 0.2 UND ATA: 0.8 DAY OF THING DATE: 0.2 UND ATA: 0.8 DAY OF THING DATE: 0.2 UND ATA: 0.8 DAY OF THING DATE: 0.2 UND ATA: 0.8 DAY OF THING DATE: 0.2 UND ATA: 0.8 DAY OF THING DATE: 0.3 DAY OF THING DATE: 0.3 DAY OF THING DATE: 0.3 DAY OF THING DATE: 0.3 DAY OF THING DATE: 0.3 DAY OF THING DATE: 0.3 DAY OF THING DATE: 0.3 DAY OF THING DATE: 0.3 DAY OF THING DATE: 0.3 DAY OF THING DATE: 0.3 DAY OF THING DATE: 0.3 DAY OF THING DATE: 0.3 DAY OF THING DATE: 0.3 DAY OF THING DATE: 0.3 DAY OF THING DATE: 0.3 DAY OF THING DATE: 0.3 DAY OF THING DATE: 0.3 DAY OF THING DATE: 0.3 DAY OF THING DATE: 0.3 DAY OF THING DATE: 0.3 DAY OF THING DATE: 0.3 DAY OF THING DATE: 0.3 DAY OF THING DATE: 0.3 DAY OF THING DATE: 0.3 DAY OF THING DATE: 0.3 DAY OF THING DATE: 0.3 DAY OF THING DATE: 0.3 DAY OF THING DATE: 0.3 DAY OF THING DATE: 0.3 DAY OF THING DATE: 0.3 DAY OF THING DATE: 0.3 DAY OF THING DATE: 0.3 DAY OF THING DATE: 0.3 DAY OF THING DATE: 0.3 DAY OF THING DATE: 0.3 DAY OF THING DATE: 0.3 DAY OF THING DATE: 0.3 DAY OF THING DATE: 0.3 DAY OF THING DATE: 0.3 DAY OF THING DATE: 0.3 DAY OF THING DATE: 0.3 DAY OF THING DATE: 0.3 DAY OF THING DATE: 0.3 DAY OF THING DATE: 0.3 DAY OF THING DATE: 0.3 DAY OF THING DATE: 0.3 DAY OF THING DATE: 0.3 DAY OF THING DATE: 0.3 DAY OF THING DATE: 0.3 DAY OF THING DATE: 0.3 DAY OF THING DATE: 0.3 DAY OF THING DATE: 0.3 DAY OF THING DATE: 0.3 DAY OF THING DATE: 0.3 DAY OF THING DATE: 0.3 DAY OF THING DATE: 0.3 DAY OF THING DATE: 0.3 DAY OF THING DATE: 0.3 DAY OF THING DATE: 0.3 DAY OF TH
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TOPOLOGY:
US-08-652-816A-46
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                                                                                                                                                                         565 CACAGAAGTICCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCTACA 624
                                                                                                                                                                                                                                TGGAGCTGAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
445 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCC 504
                                                                                                                                                                                                                                                                          TGGAGCTGAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGACACAG 684
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                                                                            CTGGACAAGGGCTTGAGTGGGAAGGAACATCATCCCTATCCTTGGTATAGCAAACTACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
CATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Codes for peptide of SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Codes for peptide of SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 280.8; DB 2;
Pred. No. 4e-79;
0; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US/07/834,539
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 53, Application US/08B00353
Patent No. 5874299
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION UNMBER: US/07/834
FILING DATE: 1992-02-05
ATTORNEX/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 1.
TELECOMMUNICATION INFORMATION
TELEPHONE: 415-543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76.3%;
96.0%;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Product
TITLE OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Sm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 41b-2-2
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
**PMCTH: 812 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 96.03
Matches 288; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
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OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 372..677
COTHER INFORMATION:
US-08-800-353-53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
                                                                                                                301 ATTATGTTTGGGGGAGCGACAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGCTCATCG 360
                                                                  242 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGGGATGTTCTC 301
                                                                                                                                                             302 ATAATTATGAGCTTTACTACTACTACATGGACGTCTGGGGCCAGGGGACAATGGTCACCG 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AGGIGCAGCIGCIGCAGICIGGGGCIGAGGIGAAGAAGACCIGGGICCICGGIAAAGGICI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76.3%; Score 280.8; DB 1; Length 812; 96.0%; Pred. No. 4e-79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Transgenic Non-Human Animals Capable of ITLE OF INVENTION: Producing Heterologous Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Codes for peptide of SEQ ID NO 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Codes for peptide of SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUBER: US/07/834,539A
FILING DATE: 1992-02-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                             5-07-834-539A-53
Sequence 53, Application US/07834539A
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
TATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 14
FELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 415-543-5043
INPORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 812 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Lonberg, Nils APPLICANT: Kay, Robert M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 96.0
Matches 288; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                     241 TGGAGCTGAGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Exon
LOCATION: 241..335
OTHER INFORMATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: Exon
LOCATION: 372..677
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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CITY: Sa
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385 AGGTCCAGCTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 444
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                                                                                                                                                                                                                                                                                         CACAGAAGTICCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                      TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGACACAG 684
                                                                                                                    CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 231, Application US/09042353
| Sequence 231, Application US/09042353
| Patent No. 6255458
| GENERAL INFORMATION:
| APPLICANT: LONDERGY Nils
| APPLICANT: Kay, Robert M. Transgenic No. 6255458-Human Animals for TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for TITLE OF INVENTION: Producing Heterologous Antibodies NUMBER OF SEQUENCES: 421
| CORRESPONDENCE ADDRESS: ADDRESSE: Two Embarcadero Center, Eighth Floor STREET: Two Embarcadero Center, Eighth Floor STREET: California
| COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CUDNITY: 1.08A

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 0/09/42,353
FILING DATE: 13-WAR-1998
CLASSIFICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
APPLICATION NUMBER: US 07/80,406
FILING DATE: 13-WAR-1992
PRIOR APPLICATION NUMBER: US 07/90,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION NUMBER: US 08/053,131
FILING DATE: 16-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/053,131
FILING DATE: 2-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/056,762
FILING DATE: 2-JUN-1993
PRIOR APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
PRIOR APPLICATION NUMBER: US 08/165,699
FILING DATE: 03-DEC-1993
PRIOR APPLICATION NUMBER: US 08/165,699
FILING DATE: 03-DEC-1993
PRIOR APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
PRIOR APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
PRIOR APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
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US-09-042-353-231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            505 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATCCCTATCCTTGGTATAGCAAACTACG
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OTHER INFORMATION: /product= "human V-HI family

US-09-042-353-221

US-09-042-353-221
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APPLICATION NUMBER: 05 MAR. 1994
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
PRIOR APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
PRIOR APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
PRIOR APPLICATION NUMBER: US 08/728,417
FILING DATE: 10-OCT-1996
PRIOR APPLICATION NUMBER: US 08/758,417
APPLICATION NUMBER: US 08/758,417
APPLICATION NUMBER: US 08/758,417
APPLICATION NUMBER: US 08/758,417
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APPLICATION NUMBER: US 08/758,417
APPLICATION NUMBER: US 08/758,417
APPLICATION NUMBER: US 08
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US-08-758-417A-79
; Sequence 79, Application US/08758417A
; Patent No. 6300129
; GENERAL INFORMATION:
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Best Local Similarity 96.0
Matches 288; Conservative
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                                                               505 crigoacaacectricacricoarceaacearcarcerarcerriceraraceaacrace 564
                                                                                                                                                                                                               241 IGGAGCIGAGCAGCCIGAGAICIGAGGACACGGCCGIGIAITACIGIGCGAGAGAICCCG 300
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                                                                                                                 181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA
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                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic Non-Human Animals Capable of
TITLE OF INVENTION: Producing Heterologous Antibodies
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Codes for peptide of SEQ ID NO 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: Can Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
GURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06185
FILING DATE: 19910828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 280.8; DB 5;
Pred. No. 4e-79;
0; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                Sequence 53, Application PC/TUS9206185 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Smith, william M.
REGISTRATION NUMBER: 1464
REFERENCE/DOCKET NUMBER: 1464
TELECOMMUNICATION INFORMATION:
TELEFAX: 415-543-9600
TELEFAX: 415-543-9600
TELEFAX: 415-543-9600
TELEFAX: 415-543-9600
TELEFAX: 415-543-9600
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TELEFAX: 415-543-9600
TELEFAX: 415-43-9600
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Best Local Similarity 96.0
Matches 288; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Exon
LOCATION: 241..335
OTHER INFORMATION:
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STRANDEDNESS: doub
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LOCATION: join(241..286, 373..677)
; OTHER INFORMATION: /note= "human V-HI family gene V-H49.8"
; SEQUENCE DESCRIPTION: SEQ ID NO: 79:
US-08-758-417A-79
                 Transgenic No. 6300129-Human Animals for Producing Heterologous Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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                                                                                                                                                                                                       COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORDY disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Serafini, Andrew T.
REGISTRATION NUMBER: 41,303
REFERENCE/DOCKET NUMBER: 014643-009030US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-0CT-1996
APPLICATION NUMBER: US 08/54,404
FILING DATE: 10-0CT-1995
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-193
APPLICATION NUMBER: US 08/165,699
FILING DATE: 13-DEC-1933
APPLICATION NUMBER: US 08/155,301
FILING DATE: 12-JUL-1993
APPLICATION NUMBER: US 08/155,301
FILING DATE: 12-JUL-1993
APPLICATION NUMBER: US 08/056,762
FILING DATE: 22-JUL-1993
APPLICATION NUMBER: US 08/053,131
FILING DATE: 12-DEC-1993
APPLICATION NUMBER: US 08/053,131
FILING DATE: 16-DEC-1993
APPLICATION NUMBER: US 08/053,131
FILING DATE: 16-DEC-1993
APPLICATION NUMBER: US 08/053,131
FILING DATE: 16-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/758,417A
FILING DATE: 02-Dec-1996
CLASSIFICATION: <Unknown>
LITLE OF INVENTION: Transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (415) 576-0200
15) 576-0300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 812 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
                                                                                                                                                                 CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (415) 576-(
INFORMATION FOR SEQ ID NO: 79
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                                                                    NUMBER OF SEQUENCES: 417
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Best Local Similarity 96.0
Matches 288; Conservative
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Best Local Similarity 96.0%; Pred. No. 4e-79;
Matches 288; Conservative 0; Mismatches 12; Indels
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LOCATION: 241..285
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MOLECULE TYPE:
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445 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCC 504
                                         CTGGACAAGGGCTTGAGTGGATGGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
                                                                             505 CTGGACAAGGGCTTGAGTGGAAGGAACGATCCTTATCCTTGGTATAGCAAACTACG 564
                                                                                                                                                                                                                                               625 IGGAGCIGAGCAGCCIGAGAICIGAGGACACGCCGIGIATIACIGIGCGAGAGACACAG 684
                                                                                                                                                             565 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCTTACA 624
                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M
TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CUDULTRY: USA
CUPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OMPRATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: DC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1991
APPLICATION NUMBER: US 07/810,279
FILING DATE: 18-MAR-1992
ATTORNEY/AGENT INPORMATION:
NAME: SMICH WILLIAM
REGISTRATION NUMBER: 30,223
REBERRANCE/DOCKET NUMBER: 14643-9-3
RELERPHONE: A15-36-2400
TELERPHONE: A15-36-2400
                                                                                                                                                                                                                                                                                                                                 US-08-053-131-61
; Sequence 61, Application US/08053131
; Patent No. 5661016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR EEG ID NO: 6: SEQUENCE CHARACTERISTICS: LENGTH: 813 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
373..678
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241..285
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NAME/KEY:
LOCATION:
FEATURE:
NAME/KEY:
COCATION:
US-08-053-131-61
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DB 1;

76.3%; Score 280.8;

Query Match

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                                                                                                   386 AGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT
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1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGACCCTGGGTCCTCGGTAAAAGGTCT
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Sequence 61, Application US/08645641

Patent No. 5719032.

GENERAL INCRRATION:

APPLICANT: Lonberg, Nils

APPLICANT: Kay, Robert M.

ITILE OF INVENITON: Producing Heterologous Antibodies

NUMBER OF SEQUENCES: 150

CORRESPONDENCE ADDRESS:

ADDRESSEE: William M. Smith

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

CITY: San Francisco

CITY: San Francisco

COUNTRY: USA

STATE: California

COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Ploppy disk

COMPUTER: IBM C Compatible

OPERATION SYSTEM: PC-DOS/MS-DOS

OSPTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/645,641

FILING DATE: 20-MAY-1996

CLASSIFICATION DATA:

APPLICATION NUMBER: US 07/904,068

FILING DATE: 23-UMY-1995

FILING DATE: 23-UMY-1995

FILING DATE: 23-UMY-1995

FILING DATE: 23-UMY-1995

FILING DATE: 23-UMY-1995

FILING DATE: 23-UMY-1995

FILING DATE: 23-UMY-1995

ATTORNEY ABENT WAIN: MAIN: MANER: SAN+TH WAIN: MANER: SAN+TH WAIN: MANER: SAN+TH WAIN: MANER: SAN+TH WAIN: MANER: SAN+TH WAIN: MANER: SAN+TH WAIN: MANER: SAN+TH WAIN: MANER: SAN+TH WAIN: MANER: SAN+TH WAIN: MANER: SAN+TH WAIN: MANER: SAN+TH WAIN: MANER: SAN+TH WAIN: MANER: SAN+TH WAIN: MANER: SAN+TH WAIN: MANER: SAN+TH WAIN: MANER: SAN+TH WAIN: MANER: SAN+TH WAIN: MANER: SAN+TH WAIN: MANER: SAN+TH WAIN: MANER: SAN+TH WAIN: MANER: SAN+TH WAIN: MANER: SAN+TH WAIN: MANER: SAN+TH WAIN: MANER: SAN+TH WAIN: MANER: SAN+TH WAIN: MANER: SAN+TH WAIN: MANER: SAN+TH WAIN: MANER: SAN+TH WAIN: MANER: SAN+TH WAIN: MANER: SAN+TH WAIN: MANER: MANER: MANER: MANER: MANER: MANER: MANER: MANER: MANER: MANER: MANER: MANER: MANER: MANER: MANER: MANER: MANER: MANER: MANER: MANER: MANER: MANER: MANER: MANER: MANER: MANER: MANER: MANER: MANER: MANER: MANER: MANER: MANER: MANER: MANER: MANER: MANER: MANER: MANER: MANER: MANER: MANER: MANER: MANER: MANER: MANER: MANER: MANER: MANER: MANER: MANER: MANER: MANER: MANER: MANER: MANER: MANER: MANER: MANER: MANER: MANER: MANER: MANER: MANER: MANER: MANER: MANER: MANER: MANER: MANER: MANER:
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REGISTRATION NUMBER: 30,23
REFERENCE/DOCKET NUMBER: 14643-000913
TELEPHONE: 415-326-2400
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 813 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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LOCATION:
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505

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566 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAACCATACA
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                                                                                                                                                                                                                                                                                                                                                                 61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 CTGGACAAGGGCTTGAGTGGATGGGATGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
                                                                                                                                                                                                                                                                                                                                                                                                          446 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCC
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Patent No. 5814318
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M
TITLE OF INVENTION: Transgenic No. 5814318-Human Animals for TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 210
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 200
                                                                          Length 813;
                                                                                                                                                                                                                    1 AGGTGCAGCTGCTGCAGTCTGGGGCTGAGGAGAAGCCTGGGTCCT
                                                                                                                                                 Indels
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COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/096,762
FILING DATE: 22-JUL-1993
CLASSIFICATION: 800
                                                                      Score 280.8; DB 1;
Pred. No. 4e-79;
0; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/904,068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 17-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Smitch, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-9-4
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 23-UUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
                                                                      Query Match
Best Local Similarity 96.0%;
Matches 288; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: One "MALE"
CITY: San Francisco
STATE: California
       US-07-853-408B-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-096-762-61
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Patent No. 5789550
APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5789650-Human Animals for TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 150
CORRESPONDENCE ADDRESS:
                                                                      Length 813;
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STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                   Query Match 76.3%; Score 280.8; DB 1; Best Local Similarity 96.0%; Pred. No. 4e-79; Matches 288; Conservative 0; Mismatches 12;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/853,408B
FILLING DATE: 19920318
CLASSIFICATION: 800
CLASSIFICATION: 800
MATTORNEY/AGENT INPORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
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SEQUENCE CHARACTERISTICS:
LENGTH: 813 Daracteristics
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| TELEPHONE: 415-326-2400
| TELEPHONE: 415-326-2402
| INFORMATION FOR SEQ ID NO: 61:
| SEQUENCE CHARACTERISTICS:
| LINGTH: 813 base pairs
| TYPE: nucleic acid
| STRANDEDNESS: single
| TOPOLOGY: linear
| MOLECULE TYPE: DNA (genomic)
| FEATURE:
| NAME/KEY: CDS
| LOCATION: 241..285
| FAATURE:
| NAME/KEY: CDS
| LOCATION: 373..678
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Search completed: July 18, 2003, 19:59:08 Job time: 20.5137 secs

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July 18, 2003, 04:46:48; Search time 1002.03 Seconds (without alignments) 10397.705 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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SUMMARIES

Description	685CT1PC101 70485 H. sapie C01867 H. sapie C01877 Homo 13189 H. sapie 13189 H. sapie 13189 H. sapie 1318078 Homo 1318078 Homo 1318078 Homo 1318078 Homo 1318078 Homo 1318078 Homo 1318078 Homo 1318078 Homo 13180775 Homo 13180775 Homo 13180775 Homo 13180775 Homo 13180775 Homo 13180778 Homo 13180778 Homo 1318078 Homo	ABG63913 Homo s AX300024 Sequer X67908 H. sapier chain variable ning region; Ig heavegion; IgG; us.
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Strausberg, R.

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Submitted (0'-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive; Room 11A03, Bethesda, MD 20892-2590, NIH-MGC Project URL: http://mgc.nci.nih.gov
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      Smith, A.
                                                                                                     Location/Qualifiers
1. .50.
Acadaism="Homo sapiens"
/isolate="patient HER(SLE)"
/db xref="taxon:9606"
/cell_line="EBV-transformed 31(+) B cell line, H2F lgG"
/tissue type="Epleen"
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Manheimer-Lory, A., Katz, J.B., Pillinger, M., Ghossein, C., and Diamond, B.
Molecular characteristics of antibodies bearing an anti-DNA-asociated idiotype
J. Exp. Med. 174 (6), 1639-1652 (1991)
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Best Local Similarity 87.7%; Pred No. 1.6e-75;
Matches 315; Conservative 0; Mismatches 41; Indels
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis Staudt
Tissue Procurement: Louis Staudt
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steven Jones, Jennifer Asno, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Letticial Hsiao, Martin Kzzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
Schain, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuydeřduyn, Marco Marra.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clone distribution: MGC clone distribution information can be foun through the I.M.A.G.E. Consortium/LLML at: http://image.llnl.gov Series: IRAL Plate: 40 Row: i Column: 16 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, GenomeScan gene prediction, Similarity but not identity to protein.
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| Organism="Homo sapiens"
| Organism="Homo sapiens"
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| Clone="MGC:31937 IMAGE:4851063"
| Lissue type="Primary B-Cells from Tonsils"
| Clone | Ib="NIH MGC 48"
| Clone | Tob="NIH MGC 48"
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11arity 86.9%; Pred. No. 2.4e-74;
Conservative 0; Mismatches 45
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                                                                                                                                                                                                                                              AF174030 420 bp mRNA linear. PRI 08-MAY-2001 Homo sapiens clone 77u-c17 immunoglobulin heavy chain variable region precursor (IgH) mRNA, partial cds.
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                                       CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT 299
                                                                   358
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Catarrhini; Hominidae; Homo.
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Pred. No. 6e-74;
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1. .>420
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Mammalia; Butheria; Primates; Catarrhini; Hominid
1 (bases 1 to 420)
Manga, and Stollar, B.D.
Immunoglobulin VH gene expression in human aging
Clin. Immunol. 93 (2), 132-142 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 420)
Wang,X. and Stollar,B.D.
Direct Submission
Submitted (02-AUG-1999) Biochemistry De
School of Medicine, 136 Harrison Ave.,
Location/Qualifiers
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     358
                         423 AGCTGGTACAGGGACTGGTTCGACCCCTGGGGCCAGGGAACCCTGGTCCACCGTCTCCTCA 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (31-OCT-1991) F.M. Raaphorst, Division of Immunology, Dept. of Immunohematology and Bloodbank, Academic Hospital Leiden, Bulding 1, E3-Q, P.O.Box 9600, 2300 Leiden, THE NETHERLANDS For related sequences see 8x52954-x52972, 8x53612-3, M37277, Schroeder H.W. Jr. et al., Proc. Natl. Acad. Sci. UGA, 87:6149(1990) & Ichihara y. et al, Eur. J. Immunol. 18:649(1988).
                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. I (basea I to 351)
Raaphorst, F.M. Timmers, E., Kenter, M.J., Van Tol, M.J., Vossen, J.M. and Schuurman, R.K.
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                                                                                                                                                                                                                                                                                                                                                                                                      Restricted utilization of germ-line VH3 genes and short diverse third complementarity-determining regions (CDR3) in human fetal lymphocyte immunoglobulin heavy chain rearrangements Eur. J. Immunol. 22 (1), 247-251 (1992)
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 TCTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
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                                                                                                                                                                                                           X62965.1 GI:37680
Ig CDR3 region; Ig heavy chain; Jh element; rearranged gene;
                                                                                                                                   HSVH31328 351 bp mRNA linear PRI H.sapiens rearranged mRNA for fetal IG heavy chain Vh3, unidentified D (or N) region and Jh4 (clone FL13-28).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12;
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/cell_type="B lymphocyte"
/tissue_type="liver"
/dev_stage="13 week old foetus"
1. 296
/note="Vh element"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32;
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.larity 87.7%; Pred. No. 2.4e-74;
Conservative 0; Mismatches 32
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/isolate="Clone FL13-28"
/db_xref="taxon:9606"
/chromosome="14"
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83 c 118 g
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/note="CDR3"
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Raaphorst, F.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
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Homo sapiens
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Matches 315; Conserv
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

[ (bases 1 to 351)
Leucht, S., Uttenreuther-Fischer, M. M., Gaedicke, G. and Fischer, P. The B cell superantigen-like interaction of intravenous immunoglobin (IVIG) with Fab fragments of V(H) 3-23 and 3-30/3-30.5 germline gene origin cloned from a patient with Kawasaki disease is enhanced after IVIG therapy

[ Lin. Immunol. 99 (1), 18-29 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSA300796 351 bp mRNA linear PRI 10-APR-2001
Homo sapiens partial mRNA for immunoglobulin gamma heavy chain
variable region (IGHV3-7), clone M2-129 (m2hie129), Kawasaki
AJ300796
                                                                                                                                                                                                                                                                                                                                                                                                                                            240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Piscus. Submission
Submitted (17-JAN-2001) Fischer P., Charite Children's Hospital,
Molecular Biology Laboratory, Humboldt-University, Ziegelstr. 5-9,
Berlin, 10117, GERMANY
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              300 CTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AJ300796.1 GI:12733998
IGHV3-7 gene; immunoglobulin gamma heavy chain; kawasaki disease;
variable region.
                                                                                                                                                                                                                                      TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA
                                                                                                                                                                                                                                                                                                       GGGAAGGGGCTGGAGTGGTGATATATATGGTAGTCGGAATTGAACCATACTATGCG
                                                                                                                                                                                                                                                                                                                                                   181 GGGAAGGGGCTGGAGTGGGTGGCCAACATAAAGCAAGATGGAAGTGAAATACTATGTG
                                                                                                    1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC
                                                                                                                                                Grecaecregaercregegegaecrregrecaeccregegegerccreageacrerec
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/gene="1GHV3-7"
/fencl="immune response"
/codon_start=1
/product="immunoglobulin gamma heavy chain variable
                                                  3;
9; Length 420;
                                                  45; Indels
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="M2-129 (m2hie129)"
/cell_type="B cell"
/rearranged
Score 261; DB 9
Pred. No. 2e-73;
0; Mismatches
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Query Match 72.9%;
Best Local Similarity 86.6%;
Matches 311; Conservative
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Fischer, P.
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HSA300796
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/tb_xref="G1:3170739"
/tb_xref="G1:3170739"
/tb_xref="G1:3170739"
/db_xref="G1:3170739"

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AF062138.1 GI:3170738
                                                           TGTGCAGCCTCTGGATTCACCTTTAGTAGCTATTGGATGAGCTGGGGTCCGCCAGGCTCCA 180
                       TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
                                                                                                                           GGGAAGGGGCTGGAGTGGGTTAATAATAATGGTAGTCGGAATTGAACCATACTATGCG 179
                                                                                                                                                         GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
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1 (Dassa 1 to 420)

Wang, X. and Stollar, B.D.

Immunoglobulin VH gene expression in human aging

Clin. Immunol. 93 (2), 132-142 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                   CTTATGACAGAGCTACTTTGACTACTGGGGCCCAGGGAACCCTGGTCACCGTCTCCTCA 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATATCGGTGACTGGTGGTTCGACCCCTGGGGCCAGGGAACCCTGGTCACCGTCCTCCTCA
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/db_xref="taxon:9606"
/chromosome="14"
/map="44912.33"
/clone="45u-11"
/cell_type="peripheral B lymphocyte"
/tissue_type="blood"
/note="from elderly repertoire 45u"
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/gene="IGH"
97.0
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/gene="IGH"
58. .>420
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/gene="IGH"
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363 bp mRNA linear PRI 02-JUL-2002 partial cds, clone:ya0116h.
                                                                                                                                    /translation="GLSWVFLVAILEGVQCEVQLVESGGGLVQPGGSLRLSCAASGFTFSSYWMSWVRQAPGKGLEWVANIKQDGSEKYYVDSVKGRFTISRDNAKNSLYLQMNSL
RAEDTAVYYCARGLTGATDAFDIWGQGTWVTVSS"
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Construction and characterization of antibody libraries: isolation of therapeutic human antibodies and application to functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                          '-1. .>409
/codon_start=2
/product="Ig heavy chain variable region (VDJ)"
/protein_id="CAA78558.1"
/db_xref="G1:31006"
/db_rief="G1:31006"
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                                                                                                                                                                                                                                                                                                                                                                                                                              72.5%; Score 259.4; DB 9 llarity 86.4%; Pred. No. 6.5e-73; Conservative 0; Mismatches 46
/tissue type="feral liver"
/clone lib="ESS"
<1. .>409
                                                                                                                                                                                                                                                                                                                                                                     67
                                                                                                                                                                                                                                           50.343
/note="Ig V-segment"
344.362
/note="Ig D-segment"
363.409
/note="Ig J-segment"
a 90 c 134 9
                                                                                                                                                                                                       1. .49
/note="signal peptide"
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2 (bases 1 to 363)
Kurosawa, Y.
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nes 310; Conserv
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                     /protein_id="CAC28901.1"
/db_xref="G1:12733999"
/tanslation="EVQLLESGGGLVQPGGSLRLSCAASGFTFGSYMMSWVRQAPGKG
LEWVANISQCSSEXTYVDSVKGRFFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDDSG
IFDYWGQGTLVTVSS"
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11 (bases 1 to 409)
Tonnelle,C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mechanisms that generate human immunoglobulin diversity operate from the 8th week of gestation in fetal liver Eur. J. Immunol. 23 (1), 110-118 (1993) 93122076
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                                                                                                                       <1. .>351
/gene="IGHV3-7"
/product="immunoglobulin gamma heavy chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (09-JUN-1992) C. Tonnelle, Centre d'Immunologie Marseille-Luminy, Case 906, 13288 Marseille Cedex 9, FRANCE (bases 1 to 409)
Cuisinier,A.M., Gauthier,L., Boubli,L., Fougereau,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       H. Sapiens rearranged Ig heavy chain variable region (VDJ). Z14189. X65741. Z14189.1 GI:31005. Ig D-segment; Ig heavy chain; Ig J-segment; Ig V-segment; Homo sapiens. Homo sapiens.
                                                                                                                                                                                                                                                                     Length 351;
                                                                                                                                                                                                                                                                  Query Match 72.8%; Score 260.6; DB 9; Length Best Local Similarity 87.2%; Pred. No. 2.6e-73; Matches 313; Conservative 0; Mismatches 34; Indels
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/db_xref="taxon:9606"
/chromosome="14"
/clone="3.14"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 351)
Leucht, S., Uttenreuther-Fischer, M. M., Gaedicke, G. and Fischer, P. The B cell superantigen-like interaction of intravenous 330/3-30.5 immunoglobin (IVIG) with Fab fragments of V(H) 3-23 and 3-30/3-30.5
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                                                                                                                                                     /organism="Homo sapiens"
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/db xref="taxon:9606"
/cell_line="EBV-transformed 31(+) B cell line,III-3R IgM"
/f.saue_type="spleen"
/lote="IgM heavy chain variable region"
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301 TGGGAGAGGTGGTTCGGGGAGTCCCCGCCTTTGACTACTGGGGCCAGGGAACCCTGGTC 360
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351 bp mRNA linear PRI 10-APR-200:
Homo sapiens partial mRNA for immunoglobulin gamma heavy chain
variable region (IGHV3-7), clone MI-45 (mihie45), Kawasaki disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 TGTGCAGCCTCTGGATTCACCTTTAGTAGCTATCGGATGAGCTGGGTCCGCCAGGCTCCA
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IGHV3-7 gene; immunoglobulin gamma heavy chain; kawasaki
variabe region.
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Pred. No. 1.4e-72;
0; Mismatches 41; Indels 14;
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and Diamond, B.
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molecular characteristics of antibodies
unti-DNA-associated idiotype
J. EXP. Med. 174 (6), 1639-1652 (1991)
                                                                                                               Location/Qualifiers
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ilarity 85.2%;
Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X63850.1 GI:38346
anti-DNA antibody; complementarity determining region; Ig heavy chain; Ig variable region; IgM;
chain; Ig kappa light chain; Ig variable region; IgM;
immunoglobulin; systemic lupus erythematosus.
Homo sapiens.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
'Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 372)
Manheimer-Lory,A., Katz,J.B., Pillinger,M., Ghossein,C., Smith,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Gaps
                                                                                                                                   1.363
/organism="Homo sapiens"
/db_xref="reaxon:9606"
/clone="ya0116h"
/clone lib="A01164"
/note="mixture of tissues:tonsils, umbilical cords,
peripheral blood and bone marrow"
Submitted (25-JUL-2001) Yoshikazu Kurosawa, Institute for Comprehensive Medical Science, Fujita Health University, Immunology; Kutsukake-cho, Toycake, Aichi 470-1192, Japan (E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387) Please visit our web aite University our web aite University (buy.fujita-hu.ac.jp/immunity/.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 258.4; DB 9; Length 363;
Pred. No. 1.4e-72;
0; Mismatches · 46; Indels 2;
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Best Local Similarity 86.5%;
Matches 308; Conservative (
                                                                                                                                                                                                                                                                                      "gene="IGH"
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Matches 314; Conservative
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DEFINITION
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PUBMED
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| Dix xref="d1:1273976"
| translation="MYQLLESGGGIVOPGESIRLSCAASGFTFSSYGMSWVRQAPGKG
| LEWVANIKQDGSEKYYVDSVKGRFTISRDNAKNSLYLQMNSIRAEDTAVYYCAREVAG
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                                                                     2 (bases 1 to 351)
Fischer, P.
Fischer, P.
Submission
Submitted (17-JAN-2001) Fischer P., Charite Children's Hospital,
Molecular Biology Laboratory, Humboldt-University, Ziegelstr. 5-9,
Berlin, 10117, GERMANY
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAAGAACTCACTGTATCTG 243
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germline gene origin cloned from a patient with Kawasaki disease enhanced after IVIG therapy Clin. Immunol. 99 (1), 18-29 (2001) 21885274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTGCAGCTGGTGCAGTCTGGGGGGGGTCTCAAGCCTGGAGGGTCCCTGAGACTCTCC
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/gene="IGHV3-7"
/product="immunoglobulin gamma heavy chain variable
                                                                                                                                                                                                                                                                                                                                                                            'product="immunoglobulin gamma heavy chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 351;
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                                                                                                                                                                                              /db_xref="Kawasaki_dissease patient".
/db_xref="taxon:9606"
/clone="M1-45 (mlhie45)"
/cell_type="B_cell"
/rearranged
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 257.4; DB 9;
Pred. No. 2.9e-72;
0; Mismatches 36;
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/gene="IGHV3-7"
/function="immune response"
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Sequence 33 from Patent WO0100678.
AX061464
                                                                                                                                                                                             /organism="Homo sapiens"
/isolate="Kawasaki disea
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Best Local Similarity 86.6%;
Matches 311; Conservative
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AX061464
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DNA linear PRI 19-FEB-1997 variable region (V3-07) gene,
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Analysis of rearranged immunoglobulin heavy chain variable region
genes obtained from bone marrow transplant (BMT) recipient
Clin. Exp. Immunol. 107 (2), 372-380. (1997)
              Human immunodeficiency virus type 1
Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate
lentivirus group.
1 (bases 1 to 375)
Watkins, B.A. and Reitz, M.S.
Human monoclonal antibodies to hiv-1 envelope glycoprotein gpi20
Patent: WO 0100678-A 33 04-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Euteleostomi;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                        /organism="Human immunodeficiency virus type 1"
/db xref="taxon:11676"
/note="VH"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 256.6; DB 6; Length 375;
Pred. No. 5.2e-72;
0; Mismatches 44; Indels 11
                                                                                                                                                                                                                          THE GOVERNMENT OF THE UNITED STATES OF AMERICA Location/Qualifiers
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Human immunodeficiency virus type 1.
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AUTHORS
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/ ... 3460
/codon start=1
/product="1gM heavy chain variable region"
/protain_id="AAB18977.1"
/db xref="2671:1673597.1"
/translation="18701485GGGLVRPGGSLRLSCAASGFTFSSFWLNWVRQAPGKG
LEWVANIQDGSEKYYVDSVKGRFTISRDNAKNSLYLQMNSLRDDDTAIYYCARGSAG
TSPRLDYWGGGTLVTVSS"
a 94 c 114 g 78 t
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Homo sapiens partial mRNA for immunoglobulin gamma heavy chain
variable region (IGHV3-7), clone M1-40 (mlhie40), Kawasaki disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGGAAGGGGCTGGAGTGGGTGGTTAATATATAGTAGTCGGAATTGAACCATACTATGCG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240 CAAATGAACAGCCTGAGAGCCGAGGACACGCGTGTATTACTGTGCGAGAGGATCTGT 299
241 CAAATGAACAGCCTGAGAGAGAGATACACGGCCATTATTACTGTGC-GAGGGTTCGG 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disease;
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Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                              . Virgen del Rocio, Immunology, 41013
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi
Bukaryota, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 354)
Leucht, S., Uttenreuther-Fischer, M.M., Gaedicke, G. and Fischer, P.
The B cell superantjagn-like interaction of intravenous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 IGIGCAGCCTCTGGATTCACCTTTAGTAGCTTTTGGCTGAACTGGGTCCGCCAGGCTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 GTGCAGCTGGTGGAGTCTGGGGAGGCTTGGTCCGGCCTGGGGGGTCCCTGAGACTCTCC
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IGHV3-7 gene; immunoglobulin gamma heavy chain; kawasaki
variable region.
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                                                                                                                         structure of eight human
                        antibodies
Immunology 102 (3), 273-280 (2001)
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            Molecular
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HSA300785
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Direct Submission

Submission

Submission

Submissed (19-NoV-1996) Immunology, Virginia Mason Research Cenfer,

1000 Seneca Street, Seattle, WA 98101, USA

Location/Qualifiers

1. .348

/ Ap xerf = "Laxon:9606"

/ Ab xerf = "abxon:9606"

/ Apromosome = "14"

/ Map="14432-q33"

/ Clone="3b2g11"

/ Cell Lype="CD19+ B cells"

/ Lissue Lype="CD19+ B cells"

/ Lissue Lype="CD19+ Peripheral blood"

/ Note="CD19+ peripheral blood B cells obtained from a bone marrow transplant recipient 90 days post transplant; clone |

1 in reference 1"

/ Gene="13-07"
                                                                                                                                                                                                                                                                                                                                                                                                                                            dgene="v3-07"

/gene="v3-07"
/note="v3-07"
/note="v3-07"
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/db_xref="d1:1791009"
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/fb_xref="d1:1791009"
/f
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Homo sapiens clone CDC-1hc IgM heavy chain variable region mRNA,
partial cds.
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Bucmo sapiens.

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi, Wammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

(bases I to 360)

Aguilera,I., Melero,J., Nunez-Roldan,A. and Sanchez,B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC
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llarity 86.6%; Pred. No. 76-72;
Conservative 0; Mismacches 33; Indels 15;
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                   immunoglobin (IVIG) with Fab fragments of V(H) 3-23 and 3-30/3-30.5 germiline gene origin cloned from a patient with Kawasaki disease is enhanced after IVIG therapy Clin. Immunol. 99 (1), 18-29 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="dl:12733974"

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GHFDYWGQGTLVYVSS"

GHFDYWGQGTLVYVSS"
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Submitted (17-JAN-2001) Fischer P., Charite Children's Hospital, Molecular Biology Laboratory, Humboldt-University, Ziegelstr. 5-9, Berlin, 10117, GERMANY
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                  'codon start=1
'product="immunoglobulin gamma heavy chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="IGHV3-7"
/product="immunoglobulin gamma heavy chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71.3%; Score 255.4; DB 9; Length 354; 86.6%; Pred. No. 1.3e-71; ive 0; Mismatches 36; Indels 12;
                                                                                                                                                                                                                     /organism="Homo sapiens"
/isolate="Kawasaki disease patient"
/db_xxef="taxon:9606"
/clone="M1-40 (mlhie40)"
/cell_type="B_cell"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        u
                                                                                                                                                                                                                                                                                                                                                                   function="immune response"
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                                                                                                                                                                                                                                                                                                                         gene="IGHV3-7"
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                                                                                                          (bases 1 to 354)
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Matches 309; Conservative
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AF062188 372 bp mRNA linear PRI 08-MAY-2001 Homo sapiens clone 48u-19 immunoglobulin heavy chain variable

LOCUS DEFINITION

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/translation="EVQLVESGGGLVQPGGSLRLSCAGSGFPFSSYWMSWVRQAPGKG
LEWVANIKQDGSEKYYVDSVKGHFTISRDNAKNSLYLQMNSLRAGDTAVYYCARARAV
RRVGTTYFDYWGQGTLVTVSSG"
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Catarrhini, Hominidae, Homo.
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/protein_id="AAC18224.1"
/db_xref="GI:3170839"
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, Boston, MA 02111, USA
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Pred. No. 2e-71;
); Mismatches 47; Indels 8;
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/tissue type="blood"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (22-APR-1998) Biochemistry De School of Medicine, 136 Harrison Ave., Location/Qualifiers
                                                                                                                                                                                                                                                         Eukaryoča; Metazoa; Chordata; Craniat Mammalia; Eutheria; Primates; Catarrh 1 (bases 1 to 372) Wang, X. and Stollar, B.D. Immunoglobulin VH gene expression in 1011. Immunol. 93 (2), 132-142 (1999) 99459182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="14"
    cds.
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region (IGH) mRNA, partial
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Wang,X. and Stollar,B.D.
Direct Submission
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                                                                                    AF062188.1 GI:3170838
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/gene="IGH"
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Best Local Similarity 85.0%;
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                                                                                                                                                                                       sapiens
                                                                                                                                                                                                                             Homo sapiens
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                                               AF062188
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BM767227 AW402613 UI-HF-BKO AGENCOURT

BM713479 TAW402311 TBQ943156

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BQ717993 BQ709776 AW403220 BQ708724 BM914366 AW403163

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BG759119 704 bp mRNA linear EST 15-MAY-2001
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                                                                                                                     mRNA sequence.
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BG756291 602713609
BG756394 AGENCOURT
BG756386 602715711
BG755960 602716437
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Maximum Match 100%
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/organism="Homo sapiens"

/db xrefe"taxon:9606"
/clone="ImAGE:48:10603"
/clone="ImAGE:48:10603"
/clone="InAGE:48:"NIH MGC_48"
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Site_2: BcoRI; cDNA made by oligo-dT priming)
Site_2: BcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size I.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH—MGC Library."
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AL551886 LI NFL006 PL2 Homo sapiens cDNA clone CS0DI061YP03 5 prime, mRNA Sequence.

AL551886 GI GI:12890261
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/tissue_type="placenta"
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//note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"

6 a 206 c 223 g 140 t 5 others
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Eukaryota; Lto 848)

I (Bases I to 848)

I Institutes of Health, Mammalian Gene Collection (MGC)

Notional Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: capabs-remail.nih.gov,

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.lln.gov

Plate: LLCMT700 row: b column: 04

High quality Sequence Stop: 778.
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llarity 86.6%; Pred. No. 2e-61;
Conservative 2; Mismatches 37; Indels
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/note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
ECORI, CDNA made by oligo-dT priming. Directionally cloned
into ECORI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       426 TAGGGGGTAACAACGACTTTGACTATTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 484
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGAGGGATCTGT
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NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Email: cgapbs-r@mail.nih.gov
CDNA Library Preparation: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLCM1705 row: f column: 03
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Pred. No. 7.6e-58;
0; Mismatches 53; Indels 3;
                                                   organism="Homo sapiens"
                                                                                xref="taxon:9606"
Location/Qualifiers
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BG756386.1 GI:14067039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 84.4%;
Matches 303; Conservative
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                 /clone="IMAGE:483867"
/clone="IMAGE:483867"
/clone=lib="NIH MGC 48"
/tissue_type="Primary B-cells from tonsils (cell line)"
/tab_host="Drimary B-cells; Vector: pdrB7; Site 1: XhoI;
/note="Organ: B-cells; Vector: pdrB7; Site 1: XhoI;
Site_2: BcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRIX/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH MGC Library."
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AGENCOURT 7983019 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6215641
BQ709359
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLCW1384 row: o column: 02
High quality sequence stop: 667.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
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Best Local Similarity 85.0%;
Matches 305; Conservative
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found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLCM1707 row: j column: 10 High quality sequence stop: 793. Location/Qualifiers
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                                             / organism="Homo sapiens"
/db_xref="teaxon:9606"
/db_xref="teaxon:9606"
/clone_lib="NIMAGE:4855682"
/clone_lib="NIMAGE:4855682"
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/tissue_type="primary B-cells from tonsils (cell line)"
/tab_host="DHINDS (phage-resistant)"
/note="Organ: B-cells, Vector: pOTB7; Site_l: XhOI;
Site_2: Ecorl; cDNA made by oligo-dT priming.
Directionally cloned into EcorlX/Ano Sites using the following 5' adaptor: GGCACGAG(G): Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH-MGC Library."
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853 bp mRNA linear EST 15-MAY-2001
602716437F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4856553 5',
mRNA sequence.
BG755960
BG755960.1 GI:140666613
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Bukaryota, Metazoa, Chordata, Catarrhini, Hominidae, Homo.

1 (bases 1 to 853)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Email: Capabe-r@mail.nih.gov
Contact: Robert Strausberg, Ph.D.
Email: cgapbe-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D. Ph.D.
CONA Library Preparation: Ling Hong/Rubin Laboratory
CONA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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llarity 84.7%; Pred. No. 1.2e-57
Conservative 0; Mismatches 40
     ity sequence stop: 790.
Location/Qualifiers
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Matches 304; Conserv
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BQ706683
AGENCOURT 7976366 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6214494
5', mRNA Sequence.
BQ706683.1 GI:21845582
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 888)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-romail.nih.gov
Tissue Procuremen: Dr. Mark Watson

CDNA Library Preparation: Rubin Laboratory
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69.1%; Score 247.4; DB 12; Length 853;
Best Local Similarity 84.7%; Pred. No. 1.2e-57;
Matches 304; Conservative 0; Mismatches 46; Indels 9;
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299
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/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dr priming. Directionally cloned
into EcoRIXXNo sites using the following 5 adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH MGC Library."
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 950)

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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                      can
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov column: 07 Plate: LLCM2381 row: column: 07 High quality sequence stop: 653.
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Pred. No. 5.8e-57;
0; Mismatches 55;
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AGENCOURT 7977239 NIH_MGC_113 Homo 15
5, mRNA Sequence.
BQ711129 GI:21850028
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Tissue Procurement: Dr. Mark Watson
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/organism="Homo sapiens"
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Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                     /db_xref="taxon:9606"
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259 c 248
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ilarity 83.8%;
Conservative
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Best Local Simil
Matches 301; C
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602712981F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4852916 5',
mRNA sequence.
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cDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MG clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM3385 row: f column: 14
High quality sequence stop: 398.
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Pred. No. 1.1e-56;
0; Mismatches 56;
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Mammalla; Butheria; Primates; Cat
1 (bases 1 to 770)
NIH-MGC http://mgc.nci.nih.gov/.
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Best Local Similarity 83.2%;
Matches 302; Conservative
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AUTHORS
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BQ708566 934 bp mRNA linear EST 16-JUL-2002
AGENCOURT 7975980 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6214806
5', mRNA Sequence.
BQ708566
                                                                                                                                        National instructs

Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausherg, Ph.D.
Contact: Robert Strausherg, Contact: Robert Instruction Contact: Robert Instruction Contact: Robert Instruction Contact: Robert Instruction Contact: Robert Instruction Contact: Robert Instruction Contact: Robert Instruction Contact: Robert Instruction Contact: Robert Instruction Contact: Robert Instruction Contact: Robert Instruction Contact: Robert Instruction Contact: Robert Instruction Contact: Robert Instruction Contact: Robert Instruction Contact: Robert Instruction Contact: Robert Instruction Contact: Robert Instruction Contact: Robert Instruction Contact: Robert Instruction Contact: Robert Instruction Contact: Robert Instruction Contact: Robert Instruction Contact: Robert Instruction Contact: Robert Instruction Contact: Robert Instruction Contact: Robert Instruction Contact: Robert Instruction Contact: Robert Instruction Contact: Robert Instruction Contact: Robert Instruction Contact: Robert Instruction Contact: Robert Instruction Contact: Robert Instruction Contact: Robert Instruction Contact: Robert Instruction Contact: Robert Instruction Contact: Robert Instruction Contact: Robert Instruction Contact: Robert Instruction Contact: Robert Instruction Contact: Robert Instruction Contact: Robert Instruction Contact: Robert Instruction Contact: Robert Instruction Contact: Robert Instruction Contact: Robert Instruction Contact: Robert Instruction Contact: Robert Instruction Contact: Robert Instruction Contact: Robert Instruction Contact: Robert Instruction Contact: Robert Instruction Contact: Robert Instruction Contact: Robert Instruction Contact: Robert Instruction Contact: Robert Instruction Contact: Robert Instruction Contact: Robert Instruction Contact: Robert Instruction Contact: Robert Instruction Contact: Robert Instruction Contact: Robert Instruction Contact: Robert Instruction Contact: Robert Instruction Contact: Robert Instruc
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    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 895)
NHH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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68.0%; Score 243.6; DB 14; Length 895;
Best Local Similarity 83.1%; Pred. No. 1.14-56;
Matches 304; Conservative 0; Mismatches 54; Indels 8;
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LOCUS
DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/dr.gr.ef="trackon:9606"
/clone=lib="WindEr:4852916"
/clone=lib="WindEr:4852916"
/clone=lib="WindEr:4852916"
/tlab_host="Drimary B-cells from tonsils (cell line)"
/tlab_host="Drimary B-cells, vector: pOTB;
/tote="Organ: B-cells, vector: pOTB;
/note="Organ: B-cells, vector: pOTB;
/site 2: EcoRi; cDNA made by oligo-dT priming.
Directionally cloned into EcoRi/Xhol sites using the policy of sorganisms.

Following 5' adaptor: GGCAGG(G) Size-selected 550bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkelsy) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).

Note: this is a NIH_MGC Library."
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
MA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Link at:
http://ange.lln.gov
Plate: LLCM1698 row: b column: 21
High quality sequence stop: 718.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human.
Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGAAGGGGCTGGAGTGGGTGGTTAATAATGGTAGTCGGAATTGAACCATACTATGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG
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Pred. No. 1.1e-56;
); Mismatches 42
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AGENCOURT 7983184 NIH_MGC_113 .
5', mRNA Sequence.
BQ710073
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EST.
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Best Local Similarity 84.4%;
Matches 303; Conservative
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BQ710073
LOCUS
DEFINITION
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ORIGIN
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225 179 285

9

Gaps

8

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                                                      BQ708029

AGENCOURT_8352453 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6277625
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 979)

NIH-MGC http://mgc.nci.nih.gov/.

NiH-MGC listic. Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC.clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCW2464 row: e column: 18
High quality sequence stop: 626.
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Pred. No. 1.7e-56;
0; Mismatches 36; Indels 1;
                                                                                                                                                                               BQ708029.1 GI:21846928
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Best Local Similarity 88.2%;
Matches 276; Conservative
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                                                                                                                  5', mRNA sequence.
BQ708029
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                                                                                                   Eukaryota.
Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 934)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov l column: 07
High quality sequence start: 6
High quality sequence stop: 653.
Location/Qualifiers
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Pred. No. 1.4e-56;
0; Mismatches 54; Indels 8;
                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
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/organism="Homo sapiens"
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Matches 304; Conservative C
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I (Dases I to 443)

S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L (Onbact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.inh.gov

ECO RI site shown at the beginning of the sequence.

Tissue Frocurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M.B. Soares Lab

CDNA Library Arrayed by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be found through the II M.A.G.B. Consortium/Lible at:

Wow-bio.linl.gov/bbrp/image.html

Seq primer: MJ Forward.ac
                                                                                                                                                                                                               AW401428 443 bp mRNA linear EST 16-FEB-2000 UI-HF-BK0-aad-b-02-0-UI.rl NIH MGC_36 Homo sapiens cDNA clone IMAGE:3053139 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 GGGAAGGGGCTGGAGTGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       424 AACAACCAGCTGGTAGATTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
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EURATYOTAS, Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Mammalia: Eutheria: Primates; Catarrhini; Hominidae; Homo.

SINIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Mational Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: capbs-remail.nih.gov

Contact: Robert Strausberg, Ph.D.

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Tissue Procurement: Louis M Staudt, M.D., Ph.D.

CDNA Library Arrayed Dy: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Clone distribution: MGC clone distribution information can be found: Liming column: O6

High quality sequence stop: 696.

High quality sequence stop: 696.

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602245420P1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4336541 5',
mRNA: sequence.
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144

204

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(0.5-1.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Butheria, Primates; Catarrhini; Hominidae, Homo.

Mammalia; Euto 540)

I (bases 1 to 540)

NIH-MCC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M.B. Soares Lab

CDNA Library Arrayed by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:

www-bio.linl.gov/bbry/image/image.html

Seq primer: M13 Forward.
                                                                                                                                                              AW402648 540 bp mRNA linear EST 16-FEB-2000 UI-HF-BK0-aav-b-10-0-UI.rl NIH MGC_36 Homo sapiens cDNA clone IMAGE:3055051 5', mRNA sequence.
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0; Mismatches 57; Indels 5;
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Db 430 ACTAGCAGCTGGTATAAACTGGTCGGACCCTGGGGCCAGGGAACCCTGGTCATCGTCTCC 489

Qy 356 TCA 358

Db 490 TCA 492
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Search completed: July 18, 2003, 09:26:12 Job time : 622.38 secs

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Human anti-HER2/ne AAV293 anti-(MCP)-DNA encoding anti-DNA encoding the h DNA encoding the h MAD 27AI heavy cha

AASO3534 AAA46866 AAA46894 ABA94334 AAS22532 AAH30055

Single chain Apo-2 Nucleotide sequenc

DP54 VH gene.

ABL41734 AAQ89332

Human cDNA encodin TRO005 heavy chain Internalising anti IN2A8 MAb heavy ch

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AAA4684 AAA46890 AAA46890 AAA46896 AAA46891 AAA46891 AAA30056 AAH30056 AAH30056 AAH31153 AAF41153

99399 99399

Human coding seque Human anti-GPID/I Human HIV-1 monocl ACZ885 antibody 2.1.1 Human anti-CD40 mo MAb 6-2 heavy chai Nuclectide sequenc DNA sequence of he DNA encoding heavy

AAF29079 ABL55674 ABK88453 ABA94330

ALIGNMENTS

RESULT 1 AAF2907

Human immunodeficiency virus-1; HIV-1; human monoclonal antibody; envelope glycoprotein; gpl20; diagnosis; ds. Human HIV-1 monoclonal antibody coding sequence SEQ 1D NO: 33. (USSH) US DEPT HEALTH & HUMAN SERVICES BP. AAF29077 standard; DNA; 375 23-JUN-2000; 2000WO-US17327. 99US-0141701 03-APR-2001 (first entry) Watkins BA, Reitz MS; WO200100678-A1 30-JUN-1999; Homo sapiens 04-JAN-2001 AAF29077;

> Anti-ILB monoclona Human anti-FAPalph Anti-FAPalpha anti Affinity matured c Affinity matured c Human clone A6 fus Human interleukin Human HIV-1 monocl Description AAF29077 AAV74274 AAH41661 AAH30007 AAK98398 AAK98407 AAK32986 ABK32986 ABK32986 ΩI 222222222 DB Length 675 675 402 788 792 794

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Query Match

Score

Result Š 256.6 254.6 243.6 243.2 241.2 240.2 240.2

Novel human monoclonal antibody immunoreactive with human immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1

WPI; 2001-112438/12. P-PSDB; AAB62776.

ONA sequence of hu

Kuerschner

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GTGCAGCTGGTGGAGTCTGGGGGGGGGTCCTGGAGGGTCCCTGAGACTCTCC
                                                                                                                                                                                                                                                                                                                       This invention describes a human antibody (hAb) against a fusion (poly)peptide or protein that includes a segment of at least 6 consecutive His residues. This antibody is useful in Western blots, enzyme-linked immunosorbent assay (ELISA), immunofluorescence or immunoprecipitation assays. Also hAb can be used for affinity purification of the protein, for in vivo diagnosis or therapy, and in production of vaccines. hAb are universally applicable alternatives to human serum. They are specific for the polyhistidine tag, regardless of the nature of the rest of the protein. Since hAb are not produced in an animal, they contain no components that can induce an immune response in humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71.1%; Score 254.6; DB 20; Length 814;
.larity 85.1%; Pred. No. 6.9e.61;
Conservative 0; Mismatches 49; Indels 5;
                                                                                                                                                                                                     Human antibody against fusion protein with polyhistidine tag -
useful as standard in immunoassays, for affinty purification,
diagnosis and therapy and for preparing vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human interleukin 8 antibody nucleotide seguence M1-23H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 814 BP; 181 A; 228 C; 232 G; 173 T; 0 other;
                                                                                  Kipriyanov
                                          (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP.
                                                                                                                                                                                                                                                                                      Claim 2; Fig 4; 20pp; German.
  97DE-1028697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAH41661 standard; DNA; 675
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                                                                                  'n,
                                                                                  M, Doersam | welschof M;
                                                                                                                                             WPI; 1999-106000/09.
P-PSDB; AAW90180.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 309; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCA 358
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  04-JUL-1997;
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                                                                                  Braunagel
Little M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGTTCGGGGAGTTATTATTTCTACCCCTTTGCCTACTGGGGCCAGGGAACCCTGGTCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCT-- 297
                                                                                                The present invention provides the protein and coding sequences for the variable regions of human monoclonal antibodies which are immunoreactive with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gpl20. These can be used in diagnosis and therapy of HIV-1 infection.
                                                                                                                                                                                                                                                                                                                                                                 99
                                                                                                                                                                                                                                                                                                                                                     GTGCAGCTGGAGGATCTGGGGGAGGCTTGGTCCCAGCCTGGGGGGTCCCTGAGACTCTCC
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                                                                                                                                                                                                                                                                                      Gaps
  HIV-1
                                                                                                                                                                                                                                                                                      11;
                                                                                                                                                                                                                                         Query Match
71.7%; Score 256.6; DB 22; Length 375;
Best Local Similarity 85.1%; Pred. No. 1.7e-61;
Matches 314; Conservative 0; Mismatches 44; Indels. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               codon given"
  passive immunotherapy to
                                                                                                                                                                                                     Sequence 375 BP; 81 A; 90 C; 116 G; 88 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human clone A6 fusion protein antibody DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3..814
/*tag= a
/note= "Partial sequence,
in biological sample and providing infected mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                             Claim 4; Page 46; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAV74274 standard; DNA; 814 BP
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298 311. 355

371

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9 71 179 191

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184 GACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTG 243 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT 299

GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG

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244 CAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAG-----

---ATGGGATAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCA 300 CITAIGACAGAGGCIACITIGACIACIGGGGCCAGGGAACCCIGGICACCGICTCCTCA

BP.

AAH30007 standard; DNA; 675

AAH30007 ID AAH3 RESULT

351

us-09-627-896b-30.rng

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The present invention describes a method for detecting an analyte in a human sample containing human antibodies that specifically bind to antibodies from a nonhuman species. The method involves contacting the sample with a human antibody (1) which specifically binds to antibodies from a nonhuman species and detecting the binding between (1) and the analyte to indicate presence of the analyte. The method is used for detecting an analyte in a human sample containing human anti-mouse antibody (HAMA) (preferably human anti-mouse idiotype antibodies and/or heterophilic antibodies). The method can also be used for detecting any type of target antigen including bacterrial, fungal and viral pathogens that cause human diseases e.g., hepatitis (A,B and C), influenza, Herpes, Glardia, Malaria, Leishmania, Staphylococcus aureus, Pseudomonas that cause human antibodies can be used as detection reagents for performing clinical diagnostic tests and for performing other in virro detection assays, including for research purposes. (1) can be used in qualitative assays designed to indicate the presence of one or more target antigen in a sample that usually correspond to indicate table amounts of antigen in the sample that usually correspond to the sensitivity limitations of the sample that usually correspond to one or more target antigens in a sample can also be carried out using (1). AAH41612 to AAH41686, and AAB993161 to the present interest.
                     Human antibody; detection; Fab; immunoglobulin; heterophilic antibody; human anti-mouse antibody; HAMA antibody; interleukin 8; IL-8; Herpes; target antigen; bacterial; fungal; viral; pathogen; human disease; hepatitis A; hepatitis B; hepatitis C; influenza; Giardia; Malaria; Leishmania; Staphylococcus aureus; Pseudomonas aeruginosa; ds. ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Detecting analyte in human sample containing human antibodies binding to nonhuman-antibodies, involves contacting sample with human antibody which binds to antibodies from nonhuman species and detecting binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC
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Pred. No. 1.1e-57;
0; Mismatches 45; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 675 BP; 151 A; 211 C; 188 G; 125 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Lonberg N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88; 135pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gray J,
                                                                                                                                                                                                                                                                                                                                                                                DIAGNOSTICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67.9%;
84.1%;
                                                                                                                                                                                                                                                                                             06-DEC-2000; 2000WO-US33042.
                                                                                                                                                                                                                                                                                                                                         99US-0456090.
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Best Local Similarity 84.1
Matches 302; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             Valkirs G,
                                                                                                                                                                                                                                                                                                                                                                              (BIOS-) BIOSITE DIAGN
(GENP-) GENPHARM INT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-374798/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 22; Page
                                                                                                                                                                                                            WO200140306-A1
                                                                                                                                                    sapiens.
                                                                                                                                                                                                                                                                                                                                         06-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Buechler J,
                                                                                                                                                                                                                                                    07-JUN-2001
                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Invention
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                                                                                                                                                    Homo
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human antibody phage display library; immunisation; transgenic animal;

99US-0157415. 99US-0453234.

02-OCT-1999; 01-DEC-1999;

(BIOS-) (GEND-)

02-OCT-2000; 2000WO-US27237.

WO200125492-A1.

12-APR-2001

Homo sapiens.

Synthetic.

immunoglobulin; interleukin 8; IL8; immunogen;

nucleotide fragment M1-23H.

antibody

Anti-IL8 monoclonal

Human; antibody;

(first entry)

19-JUL-2001

AAH30007;

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antibody phage display library (I), comprising: (1) providing a nonhuman transgenic animal (II) whose genome comprises human immunoglobulin genes; (2) isolating nucleic acids encoding human antibody chains (III) from lymphatic cells; and (3) forming a library of display packages whose members comprise a nucleic acid encoding (III) which is displayed from the package. The method is used for producing a human antibody display library, e.g., a Fab phage display library. The display method may be used to screen nucleic acids encoding antibody chains obstained from immunised nonhuman transgenic animals, and from this a population of antibodies may be prepared. Production of a human monoclonal antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Producing a human antibody phage display library comprises providing a transgenic animal whose genome comprises human immunoglobulin genes and isolating nucleic acids encoding antibody chains from lymphatic cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      display library using this method means there is no need to immunise humans with antigens, and the difficulties faced with immortalising B cells are avoided. AAH29958 to AAH30066 and AAB74994 to AAB75056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a method (M1) for producing a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 243; DB 22; Length 675; Pred. No. 1.1e-57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 675 BP; 151 A; 211 C; 188 G; 125 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                BIOSITE DIAGNOSTICS INC.
GENPHARM INT SUBSIDIARY OF MEDAREX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gray J, Lonberg N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 22; Page 92; 161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67.9%;
84.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Valkirs G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-335567/35.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Buechler J,
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Grackachedrackartracedakacardarcckachracekartcchakakartrace TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA

61 64 120

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rerecadentradarreacerreagnaceratecaraceacregical 123 GGGAAGGGGCTGGAGTGGGTGGTTAATAATGGTAGTCGGAATTGAACCATACTATGCG 179 124 GGCAAGGGGCTGGAGTGGCTGCTATATGGTATGATGGAAGTAAAACATACAATGCA 183

9 63

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same, such as inflammation and wound healing. The a coding sequence described in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    293 ------GATCTGTCTTATGACAGAGGTACTTTGACTGGGGCCAGGGAACCCTG 343
304 TGTACTGATGGTAGCTGCCCCACCATAGGCCTGGGCCAACTGGGGCCAGGGAACCCTG 363
                                                                                                                                                                                                                                                                                                                                         TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
                                                                                                                                                                                                                                                                                                                                                                                     64 TGTGCAGCCTCTGGATTCACCTTTAGTAACTATTGGATGAGCTGGGTCCGCCAGGCTCCA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                    GGGAAGGGGCTGGAGTGGTGGTTAATATATGGTAGTCGGAATTGAACCATACTATGCG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAPATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGTTCACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 GGGAAGGGGCTGGAGTGGCTGGCCAACATAAAGCAAGATGGAAGTGAAATACTATGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG
                                                                                                                                                                                                                                            1 GTGCAGCTGGTGGAGTCTGGGGGGGTCTGGAGGCTTGGAGGGTCCCTGAGACTCTCC
                                                                                                                                                                                                                                                                                           GTACAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 24; Length 788;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 241; DB 24; Length 7
Pred. No. 4e-57;
0; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 788 BP; 191 A; 212 C; 212 G; 173 T; 0 other;
                                                                                                    Page 46-47; 109pp; English
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Local Similarity 82.1%;
nes 308; Conservative (
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13
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Matches
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throughput generation and screening of a human antibody or immunoglobulin (Ig) library in yeast. The method comprises expressing a library of tester fusion proteins in yeast cells, each tester fusion protein comprises expressing a library of tester fusion protein activation domain or a DNA binding domain of a transcription activator and a tester protein having a large diversity within the library. The tester protein comprises a first polypeptide subunit (e.g. human variable heavy-chain, VH) whose sequence varies within the library, a second polypeptide subunit (e.g. human variable light-chain, VL) whose sequence varies within the library independently of the first polypeptide, and a linker peptide which links the first of second polypeptide subunits. The method is useful for generating with target antigens. The present DNA sequence represents an anti-ILB serv clone as described in the methods of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGGAAGGGGCTGGGAGTGGGTGGCCTACATAAAGCAAGAAGAGGAAGTGGAAGTAGAAATACTATGTG
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                                                                                                                                                                                                                                                                                                           tester proteins against protein, peptide or using a two-hybrid method in yeast, useful human antibodies and screening for their
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             invention relates to compositions and methods for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 240; DB 24; Length 792;
Pred. No. 7.5e-57;
0; Mismatches 45; Indels 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 792 BP; 166 A; 210 C; 247 G; 169 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                            affinity binding with target antigens
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ilarity 81.5%;
Conservative
23-JUN-2000; 2000US-0602373.
23-JUN-2000; 2000US-0602972.
23-JUN-2000; 2000US-0603658.
23-JUN-2000; 2000US-0603663.
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                                                                                                                                 CORP.
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                                                                                                                                                                                                                                                                                                                                         nucleic acid target(s)
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es 313; Conserv
                                                                                                                                 GENETASTIX
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                                                                                                                                 (GENE-)
                                                                                                                                                                                  Zhu L,
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ABK32986
ID ABK3
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WO200200729-A2.
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                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
Synthetic.
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                                                                                                                                                                                                                                            ABK32983;
            184
                                  240
                                                                                  300
                                                                                                                                  335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
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                                                                                                                                                                                                                                                                                                                                                                             Screening libraries of tester proteins against protein, peptide or nucleic acid target(s) using a two-hybrid method in yeast, useful for generating recombinant human antibodies and screening for their affinity binding with target antigens -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45; Indels 26; Gaps
                                                                                Human antibody; immunoglobulin; Ig; variable heavy-chain; VH; variable light-chain; VL; anti-ILB; interleukin-8; scFV clone; ds.
                                                        Affinity matured clone M36-8 DNA from anti-ILB scFv clone 123-36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 67.0%; Score 240; DB 24; Length 794; Best Local Similarity 81.5%; Pred. No. 7.5e-57; Matches 313; Conservative 0; Mismatches 45; Indels 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 794 BP; 166 A; 213 C; 247 G; 168 T; 0 other;
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                                                                                                                                                                                                         25-JUN-2001; 2001WO-US20542.
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23-JUN-2000; 2000US-0602972.
23-JUN-2000; 2000US-0603658.
23-JUN-2000; 2000US-0603663.
                                23-APR-2002 (first entry)
                                                                                                                                                                                                                                                                                           (GENE-) GENETASTIX CORP.
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P-PSDB; AAU75152.
                                                                                                                                                       WO200200729-A2.
                                                                                                                                                                                                                                                                                                                   Zhu L, Hua SB;
                                                                                                                     Homo sapiens.
Synthetic.
                                                                                                                                                                                 03-JAN-2002.
           ABK32986;
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The present invention relates to compositions and methods for high throughput generation and screening of a human antibody or immunoglobulin [1g) library in yeast. The method comprises expressing a library of rester fusion proceins in yeast cells, each tester fusion protein comprising either an activation domain or a DNA binding domain of a transcription activator and a tester protein having a large diversity within the library. The tester protein comprises a first polypeptide subunit (e.g. human variable heavy-chain, VI) whose sequence varies within the library, a second polypeptide subunit (e.g. human variable light-chain, VI) whose sequence varies within the library independently of the first polypeptide subunits. The method is useful for generating second polypeptide subunits. The method is useful for generating recombinant human antibodies and screening for their affinity binding with target antigens. The present DNA sequence represents an anti-lib screw soft invention.
                                                                                                                                                                     -----CTTATGACAGAGGCTACTTTGACTACTGGGGCCAG 334
                                                                                                                                                                                                                     304 AGCAGTAGCTGGTCTTACTATGATAGTAGTGGTTATTACTACCCTGACTACTGGGGGCCAG 363
CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT
                                                     Screening libraries of tester proteins against protein, peptide or nucleic acid target(s) using a two-hybrid method in yeast, useful for generating recombinant human antibodies and screening for their affinity binding with target antigens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human antibody; immunoglobulin; Ig; variable heavy-chain; VH; variable light-chain; VL; anti-ILB; interleukin-8; scFV clone; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA sequence of human anti-IL8 scFv clone 123-36.
                                                                                                                                                                                                                                                                                                                                     GGAACCCTGGTCACCGTCTCCTCA 358
                                                                                                                                                                                                                                                                                                                                                                                                                        GGAACCCTGGTCACCGTCTCCTCA 387
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23-JUN-2000; 2000US-0602972.
23-JUN-2000; 2000US-0603658.
23-JUN-2000; 2000US-0603658.
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P-PSDB; AAU75149.
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WPI; 1995-006791/01.
P-PSDB; AAR66301.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                                   334
                                                                                                                                                                                                                                          304 AGCAGTAGCTGGTCTTACTATGATAGTAGTGGTTATTACTACCCTGACTACTGGGGCCAG 363
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                                                                                                                                                                                                         -----CTTATGACAGAGGCTACTTTGACTACTGGGGCCAG
                                                    GTGCAGCTGGTGGAGTCTGGGGGGGGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC
                                                                     Gráckáchtáchadatccaáadadatragarccaácaadatcchaadachtch
                                                                                      TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA
                                                                                                       64 rerechecteredarreacerrinagiaerarragargaerregerececeaegerece
                                                                                                                         GGGAAGGGGCTGGAGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG
                                                                                                                                          124 GGGAAGGGGCTGGAGTGGCTGGCCTACATAAAGCAAGATGGAAGTGAGAAATACTATGTG
                                                                                                                                                            GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG
                                                                                                                                                                                               CAAATGAACAGCCTGAGGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT
                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     *tag= a
product= Human immunoglobulin Variable heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                     Primer, PCR, amplify; human, immunoglobulin, variable, heavy chain, cosmid; placenta; vector; pJB81, E.coli; mammalian; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "miscellaneous signal, does not conform to terminator or splice site sequence"
                                    26;
                 Score 240; DB 24; Length 795;
Pred. No. 7.5e-57;
0; Mismatches 45; Indels 2
Sequence 795 BP; 166 A; 211 C; 247 G; 171 T; 0 other;
                                                                                                                                                                                                                                                                    GGAACCCTGGTCACCGTCTCCTCA 358
                                                                                                                                                                                                                                                                               GGAACCCTGGTCACCGTCTCCTCA 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
184..638
                                                                                                                                                                                                                                                                                                                                                                                     Human immunoglobulin Vh gene #7.
                                                                                                                                                                                                                                                                                                                                   BP.
                 Query Match
Best Local Similarity 81.5%;
Matches 313; Conservative
                                                                                                                                                                                                                                                                                                                                  AAQ78945 standard; DNA; 877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93WO-JP00603
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638..640
/*tag= c
/note= "m:
                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (NISB ) JAPAN TOBACCO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     229..331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matsuda F;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-MAY-1993;
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119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           467 GGGAAGGGGCTGGAGTGGGTGGCCAACATAAAGCAAGATGGAAGTGAGAATACTATGTG 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             527 GACTOTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGGAAGGGCCTGGAGTGGTGATATATATGTGGTAGTCGGAATTGAACCATACTATGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            347 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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         - for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 67.0%; Score 240; DB 16; Length 877; Best Local Similarity 91.1%; Pred. No. 7.6e-57; Matches 266; Conservative 0; Mismatches 25; Indels 1
DNA fragment comprising human immunoglobulin Vh genes production of human immunoglobulin in mammalian hosts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 877 BP; 198 A; 207 C; 258 G; 214 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Single chain Apo-2 antibody 20E6 encoding cDNA.
                                                                                                                                   Claim 16; Page 39-40; 130pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
1..939
/*tag= a
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Location/Qualifiers

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Human, Apo-2; tumour necrosis factor receptor; TNFR; apoptosis; caspase; apoptosis; cancer; antibody; ss.
                                          Nucleotide sequence of single-chain Apo-2 antibody 20E6
  29-MAY-2002 (first entry)
                                                                                                                                                 Bacteriophage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ashkenazi AJ;
                                                                                                                                                                                                                                                                                                                                                                                     14-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                            15-MAY-1997;
09-FEB-1998;
                                                                                                                                                                                                                                                                                                                                           29-JAN-2002.
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                                                                                                                                                                                                                                                                                                                                                                   The present invention describes human Apo-2. Apo-2 can be used therapeutically to induce apoptosis in mammalian cells, and so is useful to treat conditions associated with decreased apoptosis e.g. cancer.

Apo-2 is believed to be a new tumour necrosis factor (TNP) receptor.

The cytokines can induce apoptosis, thought to be initiated by binding to TNFRs, and Apo-2 triggered caspase-dependent apoptosis. It can be used to identify agents activating Apo-2, useful to treat therapeutically (e.g. those containing immunoglobulin sequences can be therapeutically (e.g. those containing immunoglobulin sequences can be inhibit apoptosis) or diagnostically (e.g. those comprising anti-tag cantbodies). It can be used to produce antibodies which can be combined with a (particularly pharmaceutically (e.g. those comprising anti-tag cantbodies). It can be used to produce antibodies which can be combined to the used to produce antibodies which can be combined or used to produce dimeric molecules (especially homodimeric molecules comprising first and second Apo-2 antibodies). Agonistic (especially cor used to produce administered to induce apoptosis in mammalian cancer cells, and antegonistic antibodies used to block mammalian cancer cells, and antegonistic antibodies used to block antibodies may also be used diagnostically e.g. to detect Apo-2 excession in cells/tissues and in Apo-2 purification. The present correct antibody, designated 20E6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 TGTGCAGCCTCTGGATTCACCTTTAGTAGCTATTGGATGAGCTGGGTCCGCCAGGCTCCA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 GGGAAGGGGCTGGAGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 GGGAAGGGGCTGGAGTGGGTGGCCAACATAAAGCAAGATGGAAGTGAGAAATACTATGTG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGACGAAGGCAAGAACTCACTGTATCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                    Human Apo-2 polypeptide inducing apoptosis - useful to treat conditions linked with decreased apoptosis e.g. cancer, and produce antibodies to increase or decrease apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361 CAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAG 412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 67.0%; Score 240; DB 20; Length 939; Local Similarity 91.1%; Pred. No. 7.7e-57; Los 266; Conservative 0; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 939 BP; 218 A; 232 C; 287 G; 202 T; 0 other;
                                                                                                                                                 Kim KJ;
                                                                                                                                                 Chuntharapai A,
                                                                                                                                                                                                                                                                                                                                        Example 14; Fig 15B; 134pp; English.
98WO-US09704.
                                       98US-0020746
97US-0857216
                                                                                                                                            Adams CW, Ashkenazi AJ,
                                                                                                       (GETH ) GENENTECH INC.
                                                                                                                                                                                      WPI; 1999-045228/04.
P-PSDB; AAW83323.
14-MAY-1998;
                                       09-FEB-1998;
15-MAY-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 GGGAAGGGGCTGGATGGCCGACATAAAGCAAGATGGAAGTGAGAATACTATGTG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence encodes a single-chain Apo-2 antibody, designated 20EG, which is isolated from a phage library. It is believed that Apo-2 is a member of the tumour necrosis factor receptor (TNER) family. Apo-2 polypeptide is capable of triggering caspase-dependent apoptosis and activating nuclear factor-kappa B. A soluble extracellular domain of Apo-2 binds Apo-2 ligand (Apo-21). Apo-2 antibodies may be used to activate or stimulate apoptosis in cancer cells. They are therefore especially useful in the treatment of cancer, to enhance immune-mediated cell death in cells expressing Apo-2, to affinity purification of Apo-2 in specific cells, tissues or serum, and in solurces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GIGCAGCIGGIGGAGICIGGGGGAGGCTIGGTCCAGGCCTGGGGGGGTCCCTGAGACTCTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 TGTGCAGCCTCTGGATTCACCTTTAGTAGCTATTGGATGAGCTGGGTCCGCCAGGCTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGAAGGGGCTGGAGTGGTTAATATATGGTAGTCGGAATTGAACCATACTATGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acids encoding an Apo-2 ligand, useful for activating or stimulating apoptosis in cancer cells, thus especially useful in the treatment of cancer, or in enhancing immune-mediated cell death -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAG 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 67.0%; Score 240; DB 24; Length 939; Local Similarity 91.1%; Pred. No. 7.7e-57; les 266; Conservative 0; Mismatches 25; Indels 1
/*tag= a
/product= "single-chain Apo-2 antibody 20E6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 939 BP; 218 A; 232 C; 287 G; 202 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 14; Fig 15B; 68pp; English.
                                                                                                                                                                                                                           98US-0079029.
                                                                                                                                                                                                                                                                                          97US-046615P.
98US-074119P.
                                                                                                                                                                                                                                                                                                                                                                                      (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-224941/28.
P-PSDB; ABB09604.
                                                                                                US6342369-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180
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ABL41,734 standard; DNA; 939 BP.

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                                                                                                                                                                                                                                                                                                                                                             Keler T,
 RESULT 14.
AAF75589
                                                      g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       L- and H-chain DNA was amplified by PCR from Graves' orbital tissue and clones encoding autoimmune-associated immunoglobulin fragments were obtained. 2/15 clones of H chain (IgG1) genes showed homology to the germline gene DP54 (AAQ89332). The DNA (AAQ89333) and corresp. amino acid (AAR72075) sequences of the VH region of a representative clone, OF7H1.19, are provided.
361 CAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAG 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         aves' ophthalmopathy-associated monoclonal antibody - produced molecular cloning of immunoglobulin genes by PCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAAATGAACAGCCTGAGGCCGAGGACACGGCCGTGTATTACTGTGCGAGA 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGA 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 239; DB 16; Length 294; Pred. No. 1.2e-56;
                                                                                                                                                                              Graves ophthalmopathy associated immunoglobulin protein; orbital antigen; monoclonal antibody; heavy chain; H chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence 294 BP; 69 A; 66 C; 98 G; 61 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 72; 94pp; English
                                                                                                                                                                                           orbital antigen; monocional antimovariable region; autoimmunity; ss.
                                                                                                                                                                                                                                                                                                                                                                         (NICH-) NICHOLS INST DIAGNOSTICS.
                                                                  BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 91.1%;
Matches 265; Conservative
                                                                                                                                                                                                                                                                                                                     94WO-US10756
                                                                                                                                                                                                                                                                                                                                               93US-0124469
                                                                  AAQ89332 standard; DNA; 294
                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                      Rapoport
                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1995-139383/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; AAR72074.
                                                                                                                                                                                                                                                                                                                                                                                                   Mclachlan SM,
                                                                                                                                                 DP54 VH gene
                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                    22-SEP-1994;
                                                                                                                                                                                                                                                                                                                                               22-SEP-1993;
                                                                                                                                                                                                                                                              WO9508336-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Graves'
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The present invention provides the protein and coding sequences for human monoclonal antibodies which bind specifically to the HER2/neu growth factor receptor (also known as erbB2). These are designated 3-F2, 1-D2 and 2-B8. They can be used in the immunotherapy-based treatment and prognosis of cancers, particularly adenocarcinomas such as salivary gland, stomach, kidney, mammary gland, lung and squamous cell carcinomas, and ovarian cancer. The present sequence is a coding sequence of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 GGGAAGGGGCTGGAGTGGTTAATATATATGGTAGTCGGAATTGAACCATACTATGCG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTG- 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCTTATGGTTCGG 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---TCTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCC 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New human monoclonal antibody that specifically binds to growth factor receptor HER2/neu, for treating, preventing or diagnosing diseases characterized by aberrant HER2/neu expression e.g. cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGTCATGCACTGGGTCCGCCAGGCTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GTGCAGCTGGTGGAGTCTGGGGGGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     184 GACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                Human, HER2; neu, erbB2; oncogene; cancer, antibody; immunotherapy;
3-F2; 1-D2; 2-E8; growth factor receptor; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5,
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Pred. No. 1.6e-56;
0; Mismatches 59; Indels 5;
                                                                                                                                                                                                      Human anti-HER2/neu antibody 2-E8 heavy chain coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 366 BP; 80 A; 87 C; 114 G; 85 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 108; 113pp; English.
AAF75589 standard; DNA; 366 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-JUL-1999; 99US-0146313.
10-MAR-2000; 2000US-0188539.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82.48;
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                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antibody of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 82.44
Matches 299; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-168698/17.
P-PSDB; AAB72883.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MEDA-) MEDAREX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Deo Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                    10-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               299
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304 GGACTTATTATAACGGGGTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCC 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New compound that binds human monocyte chemoattractant protein-1, useful e.g. for treating inflammation, comprises immunoglobulin chains with specific hypervariable regions
                                                                                                                                                                                                                                                                                                                            Human; antibody; MCP; monocyte chemoattractant; antiasthmatic; antiallergic, antinflammatory; idiopathic thrombocytopennia; immunosuppressive; cytostatic; vasotropic; antiarteriosclerotic; antiartheumatic; antiarthitic; osteopathic; antigen-binding site; immunoglobulin heavy chain; monocyte migration; T cell migration; CC-type chemokine; eotaxin; allergy; callergic crinitis; cancer; hypersensitivity response; allergy; contact dermatitis; gene; inflammatory disease; asthma, psoriasis; COPD; osteoporosis; inflammatory bowel disease; multiple sclerosis; autoimmune disease; rheumatoid arthritis; diabetes; systemic lupus erythematosus; bone disease; osteoporosis; periodontal disease; leucocyte inflitration; restenosis; arteriosclerosis; AAV293; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Di Padova FE;
                                                                                                                                                                                                                                                                                                AAV293 anti-(MCP)-1 antibody heavy chain cDNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= a
/product= "AAV293 heavy chain protein"
/brans1 except= (pos:142.144, aa:Val)
/partia1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "No start or stop codon shown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Urfer R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (NOVS ) NOVARTIS AG.
(NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Payne TG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 21; 42pp; English.
                                                                                                                                                                                     ABK14254 standard; cDNA; 366 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JUN-2000; 2000GB-0016138.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-JUN-2001; 2001WO-EP07468.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hofstetter H,
                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-164525/21.
P-PSDB; AAU75737.
                                                       TCA 358
                                                                                         TCA 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200202640-A2
                                                                                                                                                                                                                                                          08-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hiestand P,
                                                                                                                                                                                                                        ABK14254;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAATTCACTGTATCTG 243
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react with ectaxin, are used to prevent or treat MCP-1 or ectaxin-
mediated disorders, particularly those that involve migration or
activation of monocytes and T cells, e.g. allergies (allergic rhinitis,
hypersensitivity responses, allergic context dermatitis), inflammatory
diseases (asthma, psoriasis, COPD, inflammatory bowel disease,
multiple sclerosis) autoimmune diseases of bone and cartilage
systemic lupus erythematosus), diseases of bone and cartilage
(disorders (haemolytic anaemia, idiopathic thrombocytopaemia) graft
rejection, cancers that include leucocyte infiltration, (re)stenosis,
arteriosclerosis, osteoporosis and many other diseases listed in the
specification. The present sequence represents the human AAV293
anti-(MCP) antibody heavy chain cDNA sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                              TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGGTGGGTACGCCAGGCTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 degaaadegecregagregeregecaacaragageaagaregaagregaaaracrarere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC
                                                                                                                                                                                                                                                                                                                                                          2
                                                                                                                                                                                                                                                                                                               Score 238.6; DB 24; Length 366;
Pred. No. 1.6e-56;
0; Mismatches 59; Indels 5;
                                                                                                                                                                                                                                                                               Seguence 366 BP; 78 A; 87 C; 118 G; 83 T; 0 other;
                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 82.4%;
Matches 299; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCA 358
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Run on:

Sequence:

Minimum DB Maximum DB

Database

Searched:

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GTGCAGCTGGTGCAGTCTGGGGGGAGCGTGCAGCTGGGAGGTCCCTGAGACTCTCC
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US-10-040-244-14

US-09-927-112B-89

US-09-927-121B-89

US-09-453-234-59

US-09-453-234-59

US-09-925-299-230

US-09-925-299-230

US-09-925-299-230

US-09-844-684-112

US-09-844-684-12

US-09-848-12

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US-09-848-798-91

US-09-848-798-91

US-09-848-798-77

US-09-848-798-77

US-09-848-798-88
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US-09-453-234-99
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GENERAL INFORMATION:
APPLICANT: Buechler, Joe
APPLICANT: Valkirs, Gunars
APPLICANT: Cary, Jeff
APPLICANT: Lonberg, Nils
APPLICANT: Genpharm International
TITLE OF INVENTION: Human Antibodies
FILE REFERENCE: 020015-000110US
CURRENT APPLICATION NUMBER: US/09/453,234
CURRENT APPLICATION NUMBER: US/09/453,234
CURRENT APPLICATION NUMBER: US/09/453,234
CURRENT FILING DATE: 1999-10-02
NUMBER OF SEQ ID NOS: 112
SEQ ID NO 67
LENGTH: 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 67, Application US/09453234
Publication No. US20030091995A1
GENERAL INFORMATION:
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Best Local Similarity. 84.1%;
Matches 302; Conservative
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NAME/KEY: CDS
! LOCATION: (1)..(675)
US-09-453-234-67
  TYPE: DNA ORGANISM: Homo sapiens
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63.0
63.0
62.8
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230.6
230.6
230.2
230.2
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230.2
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                                                                                                                                                                  July 18, 2003, 06:19:39; Search time 86.5438 Seconds (without alignments) 8533.875 Million cell updates/sec
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Sequence 7, Ap
Sequence 24, P
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                       GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-811.737-7
US-09-811.737-24
US-10-052-798-7
US-09-972-656-67
US-10-153-382-8
US-10-153-382-4
US-10-153-382-1
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US-10-153-382-1
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US-10-073-444-644-1
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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358
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Match Length
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119

TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA

61

Result

9 63

Gaps

12;

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61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG
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                                                                                                                                                                                                                                                                                                          Score 241; DB 10; Length 788; Pred. No. 1.7e-72; 0; Mismatches 50; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Apo-2 Receptor
NUMBER OF SEQUENCES: 14
CORRESPONDENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA WAY
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER: READABLE FORM:
MEDIUM TYPE: 3:5 inch, 1.44 Mb floppy disk
COMPUTER: IBM C compatible
OCMPUTER: BEADABLE FORM:
READABLE FORM:
COMPUTER: BEADABLE FORM:
COMPUTER: BEADABLE FORM:
APPLICATION TOWNER: US/10/052,798
Patent No. US20020099180A1

APEREAL INFORMATION:
APPLICANT: Bochringer Ingelheim Pharma KG
TITLE OF INVENTION: Human FAP-alpha-specific antibodies
TITLE OF INVENTION: Human FAP-alpha-specific antibodies
TITLE REFERENCE: 1-1129
CURRENT APPLICATION NUMBER: US/09/811,737
CURRENT FILING DATE: 2001-03-19
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIN Ver. 2.1
SEQ ID NO 24
LIENGTH: 788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULY 4
US-10-052-798-7
Sequence 7, Application US/10052798
Setulication No. US20020150985A1
GENERAL INFORMATION:
APPLICANT: Adams, Camilia W.
ARAFERZI, AVI J.
CHURTHATAPAT AND J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 67.3%;
Best Local Similarity 82.1%;
Matches 308; Conservative (
                                                                                                                                                                                                                          TYPE: DNA
CORGANISM: Homo sapiens
US-09-811-737-24
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                                                                                                                                                                                                                                      244 CAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAG------- 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGGTGGGTACGCCAGGCTCCA 119
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                                                                                    124 GGCAAGGGGCTGGAGTGGGTGGCTATATGGTATGGAAGTAAAACATACAATGCA 183
                                                                                                                            GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
                                                                                                                                                               184 GACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTG 243
                                                                                                                                                                                                            CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT 299
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    64 TGTGCAGCGTCTGGATTCACCTTCAGTAACTATGGCATGCACTGGGTCCGCCAGGCTCCA 123
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                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/09811737
Patent No. US2002099180A1
FREENRAL INFORMATION:
TITLE OF INVENTION: Human FAP-alpha-specific antibodies
FILE REFERENCE: 1-1129
CURRENT APPLICATION NUMBER: US/09/811,737
CURRENT FILING DATE: 2001-03-19
NUMBER OF SEQ ID NOS: 32
SSCTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 402
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US-09-811-737-24
'; Sequence 24' Application US/09811737
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||||||||||||||||||||||||||||364 GTCACCGTCTCA 378
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US-09-811-737-7
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243 292

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APPLICANT: Deshpande, Rajendra
APPLICANT: Deshpande, Rajendra
APPLICANT: Tsai, Mei-Mei
TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
TITLE OF INVENTION: Neutralizing Activity
FILE REFERENCE: A-799
CURRENT APPLICATION WIMBER: US/09/972,656
CURRENT FILING DATE: 2001-10-05
WUMBER OF SEO ID NOS: 135
SOFTWARE: PatentIn version 3.0
                                                                                                              120 GGGAAGGGGCTGGAGTGGTTGATATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
                                                                                                                                                                                                                                                                 124 GGGAAGGGGCTGGAGTGGCTGGCCAACATAAAGCAAGATGGAAGTGAAAATACTATGTG 183
                                                                                                                                                                                                                                                                                                                                                   GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
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       GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGGTCCCTGAGACTCTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 67, Application US/09972656; Publication No. US20030099647A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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Best Local Similarity
Matches 295; Conserv
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; LOCATION: (1)
US-09-972-656-67
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LENGTH: 672
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 ferechecereredaricacerrinagiaecraricedareaecrederececedececea 240
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Publication No. US2003009655A1
GENERAL INFORMATION:
APPLICANT: Watkins, Jeffry D.
APPLICANT: Huse, William D.
APPLICANT: Huse, William D.
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APPLICANT: Huse, William D.
APPLICANT: Huse, William
FILING DATE: 02-No. US20020150985A1-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 67.0%; Score 240; DB 15; 3
Best Local Similarity 91.1%; Pred. No. 4e-72;
Matches 266; Conservative 0; Mismatches 25;
                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/079,029
                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: MARSCHANG, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1101R2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: Linear SEQUENCE DESCRIPTION: SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 650/225-5416
TELEFAX: 650/922-9801
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 939 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-995-529-7
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                                                                                                                                                                                                                                                                               GGGAAGGGGCTGGAGTGGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
                                                                                                                                                                                                                                                                                                                                                                                                                           180 GACTCTGTGAAGGGCCGGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
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                                                                                                                  15;
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SEQUENCE 1, Application No. US20030091561A1

SEDERAL INFORMATION:
APPLICANT: Van de Winkel, Jan G.J.
APPLICANT: Van de Winkel, Jan G.J.
APPLICANT: GERITACEN, Marcus A.
APPLICANT: GERITACEN, ARNOUL F.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO
TITLE OF INVENTION: EPIDERMAL GROWTH FACTOR RECEPTOR
FILE REFERENCE: GMI-020
CURRENT RAPLICATION NUMBER: US/10/172,317
CURRENT RAPLICATION NUMBER: US 60/298,172
PRIOR PELLING DATE: 2001-06-13
PRIOR PELLING DATE: 2001-06-13
NUMBER OF SEQ ID NOS: 4

SOFTWARE FASESEQ for Windows Version 4.0

SEQ ID NO 1

LENGTH: 375
                                                                         Length 348;
                                                                                                                  45; Indels
                                                                    Ouery Match
66.2%; Score 237; DB 15;
Best Local Similarity 83.3%; Pred. No. 3.1e-71;
Matches 299; Conservative 0; Mismatches 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query March 65.9%; Score 236; DB 15; Best Local Similarity 81.5%; Pred. No. 6.9e-71; Matches 303; Conservative 0; Mismarches 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
CORGANISM: Homo sapiens
US-10-172-317-1
     LOCATION: (1)..(348)
US-10-324-493-15
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US-10-324-493-15

Sequence 15, Application US/10324493

Publication No. US20030124121A1

GENERAL INFORMATION:

APPLICANT: Pluennek, John

TITLE OF INVENTION: USE OF INTERLEUKIN-4 ANTAGONISTS AND COMPOSITIONS THEREOF

FILE REPERENCE: 3005-C

CURRENT APPLICATION NUMBER: US/09/847,816

PRIOR APPLICATION NUMBER: US/09/847,816

PRIOR APPLICATION NUMBER: 09/65,343

PRIOR APPLICATION NUMBER: 09/65,343

PRIOR PLING DATE: 2000-05-05

PRIOR APPLICATION NUMBER: 09/65,343

PRIOR PLING DATE: 2000-05-19

PRIOR APPLICATION NUMBER: 09/65,343

PRIOR PLING DATE: 2000-05-19

PRIOR PLING DATE: 2000-05-19

WUMBER OF THING DATE: 2000-02-15

SEQ ID NOS: 26

SEQ ID NOS: 26

LENGTH:...348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC
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66.3%; Score 237.4; DB 15; Length
Best Local Similarity 82.7%; Pred. No. 358-71.

Matches 297; Conservative 0; Mismatches 56; Indels
; Sequence 8, Application US/10153382; Publication No. US20030086930A1; GENERAL INFORMATION:
; APPLICANT: PFIZER PRODUCTS INC.; TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES; FILE REFERENCE: F023019A; CURRENT APPLICATION NUMBER: US/10/153,382; CURRENT FILING DATE: 2002-05-22; PRIOR APPLICATION NUMBER: 60/293042; PRIOR RILING DATE: 2001-05-23; NUMBER: OF SEQ ID NOS: 39; SOFTWARE: PALENT NOS: 39; SOFTWARE: PALENT NOS: 39; SOFTWARE: PALENT NOS: 39
                                                                                                                                                                                                                                                                                                                ; TYPE: DNA; ORGANISM: Homo sapiens
US-10-153-382-8
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CURRENT APPLICATION NUMBER: US/10/153,382
                      CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: 60/293042
PRIOR FILING DATE: 2001-05-23
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 65.1%;
Best Local Similarity 82.2%;
Matches 295; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
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184 GACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTG 243
                                                                                                 244 CAAATGAACAGCCTGAGAGGCGGAGGACACGGCTGTGTATTACTGTGCGAGAGATGGTATT 303
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                                                                                                                                                                                                304 ACTATGGTTCGGGGAGTTATGAGGACTACTTTGACTACTGGGGCCAGGGAACCCTGGTC 363
                                                                      CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAG----- 291
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TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
FILE REFERENCE: PC23019A
CURRENT APPLICATION NUMBER: US/10/153,382
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: 60/293042
PRIOR FILING DATE: 2001-05-23
NUMBER OF SEQ ID NOS: 39
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TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
FILE REFERENCE: PC23019A
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82.2%; Pred. No. 1.1e-69;
iive 0; Mismatches 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 4, Application US/10153382; Publication No. US20030086930A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/10153382; Publication No. US20030086930A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 1
                                                                                                                                                                                                                                              347 ACCGTCTCCTCA 358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 295; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 1392
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  Length 1392;
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                                                              Indels
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TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
FILE REFERENCE: PC23019A
CURRENT APPLICATION NUMBER: US/10/153,382
CURRENT PILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: 60/293042
PRIOR FILING DATE: 2001-05-23
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55;
Query Match 65.1%; Score 233; DB 15; Best Local Similarity 82.2%; Pred. No. 1.1e-69; Matches 295; Conservative 0; Mismatches 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 233; DB 15;
Pred. No. 1.1e-69;
0; Mismatches 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 12, Application US/10153382; Publication No. US20030086930A1; GENERAL INFORMATION:
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180 GACTCTGTGAAGGGCCGATTCACCATCTCCCAGGGAACGCCAAGAACTCACTGTATCTG 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 81.9%; Pred. No. 2.6e-69;
Matches 294; Conservative 0; Mismatches 56; Indels 9;
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Publication No. US20030082643A1

GENERAL INFORMATION:

APPLICANT: HUAGON, Debra

APPLICANT: van de Winkel, Jan

APPLICANT: Van de Winkel, Jan

APPLICANT: WARC

TITLE OF INVENTION: HUMAN MONCCLONAL ANTIBODIES TO FC ALPHA

TITLE OF INVENTION: HUMAN MONCCLONAL ANTIBODIES TO FC ALPHA

TITLE OF INVENTION: HUMAN MONCCLONAL ANTIBODIES TO FC ALPHA

TITLE OF INVENTION: HUMAN MONCCLONAL ANTIBODIES TO FC ALPHA

TITLE OF INVENTION: HUMAN MONCCLONAL ANTIBODIES TO FC ALPHA

TITLE OF INVENTION NUMBER: US 60/339,956

PRIOR FILING DATE: 2001-02-11

PRIOR PILING DATE: 2001-02-12

NUMBER OF SEQ ID NOS: 8

SOFTWARE: PASC FOR Windows Version 4.0

SEQ ID NO 1

LENGTH: 357

TYPE: DNA
FILE REFERENCE: 3005-C
CURRENT APPLICATION NUMBER: US/10/324,493
CURRENT FLING DATE: 2002-12-19
PRIOR PELING DATE: 2001-05-01
PRIOR FLING DATE: 2001-05-01
PRIOR FLING DATE: 2001-05-01
PRIOR FLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-19
PRIOR FLING DATE: 2000-09-19
PRIOR FLING DATE: 2001-02-15
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PATCHIN VETSION 3.0
SEQ ID NO 7
LENGTH: 354
TYPE: DNA
                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                             ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(354)
US-10-324-493-7
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US-10-073-644C-1
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; Publication No. US2030124121A1
; Publication No. US2030124121A1
; GENERAL INFORMATION:
; APPLICANT: Pluenneke, John
; TITLE OF INVENTION: USE OF INTERLEUKIN-4 ANTAGONISTS AND COMPOSITIONS THEREOF
    61 GTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 GGGAAGGGGCTGGTGGTTAATATATAGGTAGTGGAATTGAACCATACTATGCG 179
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                                                                                     GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
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                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/10153382
Publication No. US20030086930A1
GENERAL INFORMATION:
TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
FILE REFERENCE: PC23019A
CURRENT APPLICATION NUMBER: US/10/153,382
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: 60/293042
PRIOR FILING DATE: 2001-05-23
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
US-10-153-382-2
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US-10-324-493-7
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                                                                                                                                                                                                                                                                                                                                                                                                  6; Gaps
                                                                                                                                                                                                                                          Query Match 64.5%; Score 231; DB 15; Length 357; Best Local Similarity 81.6%; Pred. No. 3.6e-69; Matches 293; Conservative 0; Mismatches 60; Indels
ORGANISM: Homo sapiens
US-10-073-644C-1
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Search completed: July 18, 2003, 15:38:41 Job time : 87.5438 secs THIS PAGE BLANK (USPTO)

App Appl

Appl Appl Appl Appli Appli Appli Appl

49,

Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Minimum DB Maximum DB

Database

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Seguence 48, 1
Seguence 184,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Honjo, Taguku
APPLICANT: Matsuda, Fumihiko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
CORRESPONDENCES: 145
CORRESPONDENCE ADDRESS:
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                           Sequence
Sequence
Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUMTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYBE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastERO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,809A
FILING DATE: 10-MAX-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-MAY-1993
ATTORNEY AGENT INFORMATION:
NAME: Freemen JOHN WANDER: DCT/JP93/00603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 3;
                          PCT-US93-10555-23
PCT-US93-10555-25
PCT-US93-10555-25
US-08-134-346A-49
US-08-23-819A-9
US-08-428-197-29
US-08-428-197-29
PCT-US93-10555-29
PCT-US93-10555-31
US-09-240-274-192
US-08-259-372A-1
US-08-468-671-1
US-08-545-809A-21
US-08-545-809A-21
US-08-545-809A-21
US-08-545-809A-21
US-08-545-809A-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                   US-08-545-809A-7; Sequence 7, Application US/08545809A; Patent No. 6096878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFREENCE/DOCKET NUMBER: 0650
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human İymphoblast
CGM1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genomic DNA
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TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 877 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
 TYPE: nucleic acid
STRANDEDNESS: double
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 July 18, 2003, 09:26:19; Search time 18.9834 Seconds (without alignments) 5783.490 Million cell updates/sec
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/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd
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US-09-240-274-88
US-09-273-8354-11
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Maximum Match 100%
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seq length: 200000000
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Score

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222.6 222.2

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NS-09-240-274-89

) Sequence 89, Application US/09240274

) Sequence 89, Application US/09240274

) Patent No. 6255455

) GENERAL INFORMATION:

) APPLICATION: Stepel, Donald L.

) TITLE OF INVENTION: Rh(D)-BINDING PROPEINS AND MAGNETICALLY ACTIVATED CELL

) TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF

) TITLE OF INVENTION: BOSTON SORTING METHOD FOR PRODUCTION THEREOF

) CURRENT APPLICATION NUMBER: US/09/240,274

) CURRENT FILING DATE: 1999-01-29

) EARLIER PILING DATE: 1996-04-10

) EARLIER FILING DATE: 1996-10-11

) NUMBER OF SEQ ID NOS: 224

) SOFTWARE: PatentIn Ver: 2.0

) LENGTH: 375
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        CAAATGAACACCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAG
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; OTHER INFORMATION: anti-Rh(D) chain D15
US-09-240-274-89
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ORGANISM: Homo sapiens
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Best Local Similarity 91.1%; Pred. No. 1.4e-63;
Matches 266; Conservative 0; Mismatches 25; Indels
Best Local Similarity 91.1%; Pred. No. 1.4e-63;
Matches 266; Conservative 0; Mismatches 25; Indels
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US-09-079-029-7

US-09-079-029-7

Patent No. 6342369

GENERAL INFORMATION:

APPLICANT: Adams, Camilia W.
APPLICANT: Achtenai, Avi J.
APPLICANT: Chuntharapai, Anan
APPLICANT: Kim, Kyung J.

ITILE OF INVENTION: Apo-2 Receptor
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRES:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CORPESPONDENCE ADDRES:
ADDRESSEE: Ganentech, 1nc.
STREET: 021ifornia
COUNTRY: USA
ZIP: 94080

COUNTRY: USA
ZIP: 94080

COMPUTER: READABLE FORM:
MEDIUM TYPE: 35 inch, 1.44 Mb floppy disk
COMPUTER: BADABLE FORM:
MEDIUM TYPE: 35 inch, 1.44 Mb floppy disk
COMPUTER: NINFALING Genentech)
COMPUTER: NINFALING Genentech)
CURRENT APPLICATION NUMBER: US/09/079,029
FILING DATE: WINBER: 95,600

REGISTRATION NUMBER: 95,600

REGISTRATION NUMBER: 91101R2
TELEPAN: 650/552-981

INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTHERAN: 650/552-981

INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTHERANS SINGLE
TYPE: NUMBER: SINGLE
STRANDENNESS: SINGLE
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61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1350;
                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/157,101A
FILING DATE: 05-APR-1994
CLASSIFICATION: 530
CLASSIFICATION: NARLANA K
REGISTRATION NUMBER: 35843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63.1%; Score 225.8; DB 1;
80.5%; Pred. No. 3.1e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
           NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSE: PILLSBURY, MADISON & SUTRO
STREET: 1100 NEW YORK AVENUE, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9437/204199
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Patent No. 5808032
GENERAL INPORMATION:
APPLICANT: KURIHARA, TATSUYA
APPLICANT: MATSUKURA, SHIGEKAZU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KURIHARA, TATSUYA
MATSUKURA, SHIGEKAZU
TSURUOKA, NOBUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ARIMA, KENJI
NISHIHARA, TATSURO
                                                                                                                                                                                                                                          IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 9.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3711
TELEFAX: 202-822-0944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                    Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1350 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 63.1
Best Local Similarity 80.5
Matches 289; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 6714627 CUCH
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                     ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic acid
                                                                                                                                                                                                                                                           OPERATING SYSTEM:
                                                                                                      WASHINGTON
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APPLICANT:
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                                                                                                                                                    COUNTRY:
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                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-42U2
CURRENT PELING DATE: 1999-01-29
CURRENT PELING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER PILING DATE: 1996-04-10
EARLIER FILING DATE: 1996-04-10
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SEQ ID NOS: 224
SEQ ID NO 90
LENGTH: 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----TGTCTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTC 346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184 GACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACACTGTACCTG 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           304 ATAAAGCTATGGTCCCGATACCTTTACTACTTTGACTACTGGGGCCAGGGACCCTGGTC 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4; Length 375;
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FENTION: ANTI-HBS ANTIBODY GENES AND EXPRESSION
FENTION: PLASMIDS THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63.2%; Score 226.4; DB 4; ilarity 79.8%; Pred. No. 1.4e-59; Conservative 0; Mismatches 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: anti-Rh(D) chain D16
US-09-240-274-90
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Patent No. 5808032
GENERAL INFORMATION:
APPLICANT: KURIHARA, TATSUYA
APPLICANT: TSURUOKA, NOBUO
APPLICANT: TSURUOKA, NOBUO
APPLICANT: ARIMA, KENJI
APPLICANT: ARIMA, KENJI
APPLICANT: NISHIHARA, TATSURO
TITLE OF INVENTION: PLASMIDS THEREI
                                                                                                                            Sequence 90, Application US/09240274
Patent No. 6255455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               364 ACCGTCTCCTCA 375
364 ACCGTCTCCTCA 375
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ORGANISM: Homo sapiens
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US-08-157-101A-9
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Best Local
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Sequence 77, Application US/09240274

| Sequence 77, Application US/09240274
| Sequence 77, Application US/09240274
| Sequence 77, Application US/09240274
| Sequence 77, Application US/0924027
| TILLE OF INVENTION: SHOWN METHOD FOR PRODUCTION THEREOF
| TILLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
| FILE REFERENCE: 05596-4212
| CURRENT APPLICATION NUMBER: US/09/240,274
| CURRENT APPLICATION NUMBER: 60/081,380
| EARLIER APPLICATION NUMBER: 60/081,380
| SARLIER PLING DATE: 1998-04-10
| FARLIER PLING DATE: 1998-10-11
| NUMBER OF SEQ ID NOS: 224
| SOFTWARE: PATENTIN VET: 2.0
| SEQ ID NOS: 224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 375;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 63.0%; Score 225.4; DB 4
Best Local Similarity 79.8%; Pred. No. 2.8e-59;
Matches 296; Conservative 0; Mismatches 65
Matches 296; Conservative 0
                                  CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER PLILING DATE: 1998-04-10
EARLIER PLILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PATENTIN Ver. 2.0
LENGTH: 375
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US-09-240-274-91
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OTHER INFORMATION: anti-Rh(D) chain D01
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 91, Application US/09240274

Patent No. 6254555

Patent No. 625456

Patent No. 625456

Patent No. 725462

Patent No. 725462

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Patent No. 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 80.5%; Pred. No. 3.2e-59;
Matches 289; Conservative 0; Mismatches 67; Indels 3;
               ANTI-HBS ANTIBODY GENES AND EXPRESSION PLASMIDS THEREFOR
TITLE OF INVENTION: ANTI-HBS ANTIBODY GENES AND EXPRITILE OF INVENTION: PLASMIDS THEREFOR NUMBER OF SEQUENCES: CORRESPONDENCE SIDENCES: ADDRESSE: ADDRESSE: ADDRESSE: PILLEBURY, MADISON & SUTRO STREET: 1100 NEW YORK AVENUE, N.W. CITY: WASHINGTON STATE: D.C. COUNTRY: USA ZATE: D.C. COUNTRY: USA ZATE: D.C. COMPUTER: READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IEM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PACHOLIN Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/157,101A FLILNG DATE: 05-APR-1994 CLASSIFICATION: S30 ATTONEY/AGENT INPORMATION: NAME: 35843 REFERENCE/POCKET UNBER: 35843 REFERENCE/POCKET UNBER: 35843 REFERENCE/POCKET UNBER: 35843 TELECOMMULICATION INPORMATION: TELECOMMULICATION INPORMATION: TELECOMMULICATION INPORMATION: TELECOMMULICATION INPORMATION: TELECOMMUNICATION INPORMATION:
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TELEFAX: 202-822-v..
TELEFX: 6714627 CUCH
TELEFX: 6714627 CUCH
SEQUENCE CHARACTERISTICS:
LENGTH: 1576 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
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; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-157-101A-6
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US-09-240-274-91
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                                                                                                                                          184 GAGTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAACTCCAAGAACACACTGTATCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 22, Application US/08652816A
Patent No. 587215
GENERAL INFORMATION:
APPLICANT: OSbourn, JK
APPLICANT: Allen, DJ
APPLICANT: McCafferty, JG
TITLE OF INVENTION: Specific binding members, materials and TITLE OF INVENTION: methods.
NUMBER OF SEQUENCE: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                  240 CAAATGAACAGCCTGAGAGCCGAGACACGGCCGTGTATTACTGTGCGAGA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/65,816A
FILING DATE: U3-MAY-1996
RIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.8
FILING DATE: 02-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206312.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US. 08/244,597
FILING DATE: 01-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/33308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/GB92/02240 FILING DATE: 02-DEC-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: 111inois
COWUTRY: United States of America
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: GB 9206372.6
FILING DATE: 23-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9525004.9
FILING DATE: 07-DEC-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UMBER: GB 9610824.6
23-MAY-1996
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PRIOR APPLICATION DATA:
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APPLICAT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D) -BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORITING METHOD FOR PRODUCTION THEREOF
TITLE OF INVENTION: SORITING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER FILING DATE: 1998-01-11
NUMBER OF SEQ ID NOS: 224
SOUTHWARE: PATCHILING VEY: 2.0
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                                                                                                                                                                      1 GIGCAGCIGGIGGAGICTIGGGGAGGCTIGGICAAGCCIGGAGGGICCCIGAGACTCTCC
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                                                                  DB 4; Length 375;
                                                                                                                    Indels
                                                                                      Pred. No. 4.3e-59;
0; Mismatches 62
                                                                  Score 224.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 88, Application US/09240274
Patent No. 6255455
                                                               62.8%;
79.6%;
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                                                             Query Match 62.8
Best Local Similarity 79.6
Matches 296; Conservative
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ORGANISM: Homo sapiens
US-09-240-274-77
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US-09-240-274-88
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                                           64 TGTGCACCGTCTGGATTCGTCTTCAGGAGTTATGGCATGCACTGGGTCCGCCCAGACTCCA 123
                                                                                                                   GGGAAGGGGCTGGAGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
                                                                                                                                                                         124 GGCAAGGGGCTTGAGTGGGTGTCACTTATATGGCATGATGGAAGTAATAGATTCTATGCA 183
                                                                                                                                                                                                                                      180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Irie, Reiko F
171LE OF INVENTION: HUMAN B-LYMPHOBLASTOID CELL LINE
171LE OF INVENTION: BECKETING ANTI-GANGLIOSIDE ANTIBODY
NUMBER OF SEQUENCES: 1
CORRESPONDENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSE: Pome, Smith, Lande & Rose
STREET: 2029 Century Park East, Suite 3800
CONTY: Los Angeles
STATE: California
CONTY: Los Angeles
STATE: California
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: BEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BEADABLE FORM:
MPSIGN TYPE: CALIFORNIA: PC-DOS/MS-DOS
SOFTWARE: WORDER: US 07/609803
FILING DATE: 05-NOV-1990
ATTORNEY/AGENT INFORMATION:
FLING DATE: 05-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Oldenkamp, David J
REFERENCE/DOCKET NUMBER: 94268
TELECOMMUTICATION NUMBER: 94268
TELECOMMUTICATION NUMBER: 94268
TELECOMMUTICATION NUMBER: 94268
TELECOMMUTICATION NUMBER: 91078
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CELL TYPE: Epstein Barr Virus Transformed B cell
CELL INE: L612
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NAME/KEY: CDS
LOCATION: 1..432
OTHER INFORMATION: /function= "Heavy Chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08026320A; Patent No. 5419904; GENERAL INFORMATION:
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US-09-202-181-3
IS-209-202-181-3
Sequence 3, Application US/09202181
Sequence 3. Application US/09202181
Sequence 3. Application US/09202181
Sequence 3. Application US/09202181
Sequence 3. Application US/09202181
TITLE OF INVENTION: HUMBER 12
TITLE OF INVENTION: HUMBER 105/09/202,181
CURRENT FILING DATE: 1998-12-10
PRIOR PELICATION NUMBER: 118625
PRIOR FILING DATE: 1996-06-11
PRIOR PILING DATE: 1996-06-11
PRIOR FILING DATE: 1997-06-10
NUMBER OF SEQ ID NOS: 4
SOFTWARE PACENTION OF: 2
LEOTHWAIL SASTANDER
SEQ ID NO 3
LENGTH: 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCCAGGCTCCA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 TGTGCAGCCTCTGGATTCACCTTTAGCAGCTATGCCATGAGCTGGGTCCGCCAGGCTCCA 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184 GACTCCGTGAAGGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTG 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAAATGAACAGCCTGAGAGCCGAAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   244 CAAATGAACAGCCTGAGAGGCGGACACGGCTGTGTATTACTGTGCGAGAG------ 295
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                                                                                                                                                                                                                                                                                               Query Match 62.4%; Score 223.4; DB 2; Length 3
Best Local Similarity 80.5%; Pred. No. 1.1e-58;
Matches 289; Conservative 0; Mismatches 61; Indels
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62.3%; Score 223; DB 4; Length 36
Best Local Similarity 79.9%; Pred. No. 1.5e-58;
Matches 287; Conservative 0; Mismatches 70; Indels
TELECOMMUNICATION INFORMATION:
TELEBHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 354 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                       ; TOPOLOGY: linear
US-08-652-816A-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY: CDS
; LOCATION: (1)..(363)
US-09-202-181-3
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ORGANISM: human
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TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Simi
Matches 294;
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/standard_name= "HuMab L612 Heavy Chain Variable
Region Sequence"
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                                                                                                                                                                                                                                                                                                                                             Length 432
                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Cirino, Nick M
APPLICANT: Jackson, Paul J
APPLICANT: Lehnert, Bruce E
TITLE OF INVENTION: Disruption of Anthrax Toxin Binding to C
TITLE OF INVENTION: Receptors
FILE REFERENCE: S. 89, 662
CURRENT FILING DATE: 1999-03-22
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                             69; Indels
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OTHER INFORMATION: /product= "Immunoglobulin Variat OTHER INFORMATION: /standard_name= "HuMab L612 Hear OTHER INFORMATION: Region Sequence"

PEATURE:
NAME/KEY: misc_feature
LOCATION: 148..162
OTHER INFORMATION: /function= "Complementary OTHER INFORMATION: determining region 1 (CDR1)"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 271..300
OTHER INFORMATION: /function= "Complementary OTHER INFORMATION: /function= "Complementary OTHER INFORMATION: /function= "Complementary OTHER INFORMATION: /function= "Complementary OTHER INFORMATION: determining region 2 (CDR2)"
FEATURE:
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80.5%; Pred. No. 3.4e-58;
ive 0; Mismatches 58;
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Patent No. 6329156
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Best Local Similarity 80.5
Matches 289; Conservative
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Matches 287; Conservative
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CORGANISM: Homo sapiens
US-09-273-839A-11
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US-09-273-839A-11
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GENERAL INFORMATION:

APPLICAMT: Siegel, Donald L.

APPLICAMT: Siegel, Donald L.

TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL

TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF

FILE REFERENCE: 09596-42U2

CURRENT APPLICATION NUMBER: 60/940,274

CURRENT FILING DATE: 1999-01-29

EARLIER APPLICATION NUMBER: 60/081,380

EARLIER FILING DATE: 1998-04-10

EARLIER FILING DATE: 1996-10-11

NUMBER OF SEQ ID NOS: 224

SOFTWARE: PALENTING VET. 2.0

SEQ ID NO 92

LENGTH: 375
                                                                                                                                                            225
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; Patent No. 6255455
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ilarity 79.0%; Pre
Conservative 0;
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297 -----TGTCTTATGACAGAGGCTACTTTGACTACTGGGGGCCAGGGAACCCTGGTC 346
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TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-402
CURRENT APPLICATION NUMBER: US/09/240,274
EARLIER FILING DATE: 1999-01-29
EARLIER FILING DATE: 1999-04-10
EARLIER FILING DATE: 1998-04-10
EARLIER FILING DATE: 1996-10-11
NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER: 61/028,550
EARLIER FILING DATE: 1996-10-11
SOFTWARE: PALCHIN VOR: 224
SOFTWARE: PALCHIN VOR: 2.0
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; OTHER INFORMATION: anti-Rh(D) chain D13
US-09-240-274-87
                                                                                                                                                                                                                                                                                                    Sequence 87, Application US/09240274 Patent No. 6255455 GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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US-09-240-274-87
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Search completed: July 18, 2003, 19:59:09 Job time : 19.9834 secs